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SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: Art Unit: Phone Number 30 Mail Boy and Bld Day Phone Number 30	Examiner #:	Date:
Mail Box and Bldg/Room I costing	Serial Number:	
Mail Box and Bldg/Room Location:	_ Results Format Preferred (cir	cle): PAPER DISK E-MA
If more than one search is submitted, please pr		
Please provide a detailed statement of the search topic, and de Include the elected species or structures, keywords, synonyms utility of the invention. Define any terms that may have a speknown. Please attach a copy of the cover sheet, pertinent claim	escribe as specifically as possible the	**************************************
Title of Invention:		
Inventors (please provide full names):		
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Earliest Priority Filing Date:	<u> </u>	
For Sequence Searches Only Please include all pertinent inform ppropriate serial number.	ation (parent, child, divisional, or issue	ed patent numbers) along with the
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Type of Search NA Sequence (#)	Vendors and cost w	
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Online Time:

PTO-1590 (8-01)

Other

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BioTech-Chem Library Search Results Feedback Form (Optional)



The search results generated for your recent request are attached. If you have any questions or comments (compliments or complaints) about the scope or the results of the search, please contact *the BioTech-Chem searcher* who conducted the search *or contact*:

Mary Hale, Supervisor, 308-4258 CM-1 Room 1E01

Volun	tary Resu	lts Feed	lback	Form
► I	am an ava	minan in	Worker	

Other Comments:

	1 am an examiner in workgroup. (Example: 1010)
A	Relevant prior art found, search results used as follows:
	102 rejection
	103 rejection
	Cited as being of interest.
	Helped examiner better understand the invention.
	Helped examiner better understand the state of the art in their technology.
	Types of relevant prior art found:
	Foreign Patent(s)
	Non-Patent Literature (journal articles, conference proceedings, new product announcements etc.)
	Relevant prior art not found:
	Results verified the lack of relevant prior art (helped determine patentability).
	Search results were not useful in determining patentability or understanding the invention.

Drop off completed forms at the Circulation Desk CM-1, or send to Mary Hale, CM1-1E01 or e-mail mary.hale@uspto.gov.

```
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
```

Run on:

OM protein - protein search, using sw model

February 8, 2003, 10:28:18; Search time 14 Seconds (without alignments) 34.334 Million cell updates/sec

US-09-251-073A-16 23

1 BILDV 5 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 segs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 5

Post-processing: Minimum Match 100% Maximum Match 100% Listing first 100 summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

.Description G Query Score Match Length DB

Result No.

No matches found

Search completed: February 8, 2003, 10:30:21 Job time : 14 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

February 8, 2003, 10:25:23; Search time 11 Seconds (without alignments) 18.853 Million cell updates/sec

Run on:

US-09-251-073A-16 23 1 BILDV 5

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

0

Minimum DB seq length: 0 Maximum DB seq length: 5

Post-processing: Minimum Match 100% Maximum Match 100% Listing first 100 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ü Query Score Match Length DB Result No.

Description

Search completed: February 8, 2003, 10:29:25 Job time : 11 secs

No matches found

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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February 8, 2003, 10:27:53 ; Search time 28 Seconds (without alignments) 36.794 Million cell updates/sec
OM protein - protein search, using sw model
                                                   Run on:
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US-09-251-073A-16 23 Title: Perfect score: Sequence:

1 EILDV 5

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

671580 segs, 206047115 residues Searched:

0 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 5

Post-processing: Minimum Match 100% Maximum Match 100% Listing first 100 summaries

SPTREMBL 21:*

Database :

plant:*
sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:* sp_archea.*
sp_bacteria.*
sp_fungl:*
sp_human.*
sp_invertebrate:*
sp_mammal:*
sp_mammal:*
sp_organelle:*
sp_bhage:* 12:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp archeap:*

SUMMARIES

Query Score Match Length DB

Description

No matches found

Search completed: February 8, 2003, 10:30:00 Job time : 28 secs

OM protein - protein search, using sw model

8, 2003, 10:25:08 ; Search time 33 Seconds February Run on:

(without alignments) 20.189 Million cell updates/sec

US-09-251-073A-16 23

1 BILDV 5 score: Seguence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

908470 segs, 133250620 residues Searched:

11 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 5

Listing first 100 summaries Post-processing: Minimum Match 100% Maximum Match 100%

Database

A_Geneseq_101002: :_/SIDS2/gcgdata

/SIDS2/gcgdata/geneseq/geneseqm-emb1/AA1993.DAT:* /SIDS2/gcgdata/geneseq/geneseqm-emb1/AA1994.DAT:* .DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989 /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1990 /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1991 /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1992 /gcgdata/geneseq/geneseqp-embl/AA1980.

/SIDS2/gcgdata/geneseg/genesegp-emb1/AA1997.DAT:* /SIDS2/gcgdata/geneseg/genesegp-emb1/AA1998.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:* /SIDS2

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		,			SOUTHWANTED		
Result		Query				-	
No.	Score	Match	Match Length DB	DB	ID	_	Description
-	23	100.0	2	17	AAR95719	 	Alpha-4Beta-1 inte
7	23	100.0	S	18	AAW25192	_	LDV-peptide capabl
e	23	100.0	2	19	AAW46318		Peptide recognised
4	23	100.0	ß	20	AAY03855		Integrin ligand di
S	23	100.0	S	21	AAY80488	_	Cell adhesion pept
9	23	100.0	ហ	21	AAY77442		Fibronectin CS1-de
7	23	100.0	S	21	AAY69619		VLA-4 inhibitor pe
80	23	100.0	ın	22	AAB73465	-	Fibronectin VLA-4
đ	23	100.0	'n	22	AAB91966		Fibronectin fragme
10	23	100.0	ď	22	AAB50876		Integrin recogniti

AAB59135 22 S 100.0 23 1

Peptide #3 recogni

ALIGNMENTS

RESULT 1 AAR95719

AAR95719 standard; peptide; 5 AA.

AAR95719;

04-DEC-1996 (first entry)

Alpha-4Beta-1 integrin binding inhibitory peptide 16.

VCAM-1; vascular cell adhesion molecule-1; VLA-4; very late antigen-4; inhibitor; binding; white blood cell; migration; capillary wall; tissue damage; injury; fibronectin; extracellular matrix glycoprotein; CS1; CS5; H1; LDV; active site.

Synthetic.

Location/Qualifiers /note= "Val-NH2" Key Modified-Bite

US5510332-A

23-APR-1996

94US-0271830. 07-JUL-1994;

94US-0271830. 17-JUL-1994;

(TEXA-) TEXAS BIOTECHNOLOGY CORP.

Vanderslice P; Ren K, Kogan TP, Beck PJ,

WPI; 1996-221274/22.

New peptide(s) based on the LDV domain of fibronectin - used for inhibiting binding of alpha-4, beta-1 integrin to VCAM-1, fibronectin or invasin

Disclosure; Column 21-22; 35pp; English.

DAT:

/SIDS2/gcgdata/geneseg/genesegp-emb1/AA1995.DAT: /SIDS2/gcgdata/geneseg/genesegp-emb1/AA1996.DAT:

Surface of endothelial cells that line the interior wall of capillaries ourface of endothelial cells that line the interior wall of capillaries. OverAM-1 recognises and binds to the integrin alpha-debeta-1 (14AB1) or VCAM-1 according to the antigon-4), a beterodimentic protein present on the surface of certain white blood cells to adhere to the capillary wall in areas where the tissue surrounding the capillary has been infected or damaged. Sometimes this white blood cells no adhere to an become uncontrolled, with white blood cells flooding to the scene, causing widespread tissue damage. Cops. capable of bloocking this process may be beneficial as therapeutic agents. In AHB1 also recognises the extracellular matrix glycoprotein fibronectin. Three distinct IA4B1-binding sites have been identified with ibbronectin. One site is found in the HeplI region and is expressed in all isoforms; two others (CS1 and CSS) are present in the alternatively spliced type III connecting segments. CS1 has the higher affinity for IA4B1 and contains the tripopiede LDV as its minimal active site. Peptides AAR95704-805 are modeled after a portion of the CSI peptide that include the LDV domain presented in such a way by its movel flanking sequence to produce a potent inhibitor of IA4B1 binding.

5 AA; Sequence

74400

Gaps ô Query Match 100.0%; Score 23; DB 17; Length 5; Best Local Similarity 100.0%; Pred. No. 7.8e+05; Matches 5; Conservative 0; Mismatches 0; Indels

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penton base protein; coat proteins; adenovirus; binding site; cellular adhesion; extracellular matrix molecule; binding domain; cell surface binding site; bispecific molecule; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY03855 standard; peptide; 5 AA
                                                                                                  96US-0634060.
                                                                                                                     94US-0303162.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Conservative
                                                                                                                                                                                       WPI; 1998-119984/11.
                                                                                                                                        GENV-) GENVEC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                     5 AA;
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                                                           US5712136-A
                                                                               27-JAN-1998
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Wickham TJ;
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                                                                                                                                                                                                                                                                                                                                                                                              AAW25187-W25192 are peptides containing an LDV sequence or equivalent. The peptides are capable of binding to cell adhesion molecules and are used in aqueous irrigation solutions for use during and after endoscopic operations. Preferred irrigation solutions are electrolyte-free and contain 1 microg/ml to 100 mg/ml of one or more oligopeptides containing the amino acid sequences: RGD, LDV, DGBA, GPRP, VTL, YIGSR, KGAGDV and/or REDV (given in one letter amino acid during and after tumour removal by transurethral resection. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                               LDV; leucine; aspartic acid; valine; cell adhesion molecule;
binding; bladder irrigation; tumour removal; endoscopic operation;
transurethral resection; cancer; neoplasia.
                                                                                                                                                                                                                                                                                                                                                Endoscopic irrigation solns. - contg. peptide(s) that bind to cell adhesion molecules
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fibrinogen; integrin; alpha-IIb-beta3; cell surface receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 23; DB 18; Length 5; 100.0%; Pred. No. 7.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                              LDV-peptide capable of binding cell adhesion molecules.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptides protect against recurrence of tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide recognised by integrin alpha4etal.
                                                                   AAW25192 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW46318 standard; Protein; 5 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                             Claim 6; Page 8; 8pp; German.
                                                                                                                                                                                                                                                                    95DE-1029909
                                                                                                           (first entry)
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Best Local Similarity
Then 5; Conserve
                                                                                                                                                                                                                                                                                      (FREP ) FRESENIUS AG
                                                                                                                                                                                                                                                                                                                              WPI; 1997-133793/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 AA;
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                                                                                                                                                                                                                                                 15-AUG-1995;
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             EILDV
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                                                                                                                                                                                       Synthetic
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ID AAW4
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The present sequence is a linear stretch of amino acids (present in fibronectin) recognised by the integrin alpha4betal. Integrins are cell bronectin) recognised by the integrin alpha4betal. Integrins are cell brones. The integrins of the cast proteins of adenoviruses binds to integrins. The integrins not only proteins of adenoviruses binds to integrins. The integrins not only proteins of adenoviruses binds to the extracellular matrix molecules. The mediate cellular adhesion to the extracellular matrix molecules. The acell in vitro having a particular cell surface binding site. The acell in vitro having a particular cell surface binding site. The adenovirus and a second component that selectively binds a binding domain of the penton base protein of the adenovirus and a second component that selectively binds the cell surface binding site. A complex of the adenovirus and the cell surface binding site. A complex of the adenovirus and the cell is contacted with it to allow entry of the adenovirus into the cell. The methods can be used for research and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Integrin-ligand; dissociator; disaggregation; platelet thrombus; stroke; fibrinogen; glycoprotein IIb-IIIa; angina; myocardial infarction; bone; osteoclast; osteoporosis; angiogenesis; cancer; diabetic retinopathy; psoriasis; tumour; atherosclerosis; inflammatory bowel disease; asthma; organ transplant rejection; arthritis; ILD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                   Methods for introducing adenovirus into cells - used for genetic engineering and gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
Bruder JT, Kovesdi I, McVey DL, Roelvink PW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 23; DB 19; Length 5; 100.0%; Pred. No. 7.8e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                       Claim 27; Column 2; 56pp; English.
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                                                                                                                                                                                                                                           in existing platelet thrombus in a blood vessel is due to dissociation of fibrinogen from glycoprotein IIb-IIIa. This dissociation is caused by the binding of an integrin-ligand dissociation transfer an existing platelet thrombus in a blood vessel, where the platelet comprises an existing platelet thrombus in a blood vessel, where the platelet comprises administering a compound which dissociates fibrinogen bound to a first attention platelet glycoprotein IIb-IIIa, by binding to a second interacting attention platelet glycoprotein IIb-IIIa, by binding to a second interacting attention in method is used to treat humans with unstable angina, stroke and/or acute myocardial infarction. The methods can be used to enact de-adhesion of osteoclasts from the bone surface to halt bone loss in a patient with osteoporcesis. The methods can also be used for the de-adhesion of angiogenic endothelial cells in a patient with osteoporcesis. The methods can also be used for the de-adhesion of angiogenic endothelial cells in a patient with osteoporcesis. The methods can also be used for the dissolution of pre-tormed platelet tumours, atherosclerosis, inflammatory conditions, e.g. arthritis, inflammatory bowel disease, or organ transplant rejection, and aethma. The methods can be used for the dissolution of pre-formed platelet aggregates, which is a departure from the current strategy of treatment prior to formation of vascular occlusions.
                                                                                                                                                                                                                                   The invention relates to integrin ligand dissociators. Disaggregation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bone regenerative; osteopathic; osseous tissue; reconstitution; scaffold matrix; bone formation promoter; bone resorption inhibitor; cell adhesion; osteoblast; osteoclast; bone defect; fracture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dissociator (ILD) that can be used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 23; DB 20; Length 5; 100.0%; Pred. No. 7.8e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                        Disaggregating a ligand:integrin receptor complex
                                                                                                                                                                                                       Disclosure; Page 10; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY80488 standard; peptide; 5 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US16800.
                            98WO-US18305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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ses 5; Conserv
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                            03-SEP-1998;
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 11-MAR-1999.
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Matches
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The invention relates to a novel system for reconstitution of osseous tissue comprising a scaffold carrying a compound (1) that promotes bone tormation and accomponent that decreases bone resorption (II).

(I) induces migration and adhesion of osteoblasts and osteoclasts and costeoclasts and osteoclasts and costeoclasts and selected from: selectin or selectin binding matrix. (1) is preferably selected from: selectin or selectin binding plasminosen activator inhibitors, procease inhibitors and matrix procease inhibitors and metalloprocease inhibitors. The peptides AAY80466-Y80492 are claimed examples of cell adhesion peptides used in the system of the invention. Tractures, fissures or bene mass loss: Incorporation of (1) into the scaffold results in rapid seeding by osteoblasts and the development of an organic matrix, i.e. the preformed scaffold replaces the rate-determining step of extracellular matrix formation. The scaffold can be designed to have a predetermined resorbion/degradation rate, and may include regulatory compounds for specific cell types.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fibronectin, FN; CS-1; endothelial cell; VLA-4 integrin; alpha-4-beta-1; CD49d/CD29; leukocyte; inflammatory cell; inflammation; cell adhesion; inhibitor; peptidomimetic; autoimmune disease; inflammatory disorder.
                                                                                                                                                                     System for reconstructing osseous tissue, useful e.g. for treating fractures, comprises scaffold containing promoter of bone formation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaрв
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 23; DB 21; Length 5; 100.0%; Pred. No. 7.8e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Huyghe BG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                He Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                         (PHAR-) PHARMACAL BIOTECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaeta FCA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fibronectin CS1-derived peptide #33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY77442 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                               Claim 14; Page 32; 44pp; English
                                                                                                                                                                                                                        inhibitor of bone resorption
98US-0122348.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-US26605.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 100.
nes 5; Conservative
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                                                                                                                              WPI; 2000-195084/17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200002903-A1.
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24-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-DEC-1998;
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                                                                                     Budny JA;
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Matches
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Arylalkyl and arylureidoalkyl azolylalkanoic acid derivatives
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                                                                                                                                                                                                                                            (e.g., multiple sclerosis), allergies atherosclerosis, colitis, diabetes, inflammatory bowel disease, kidney inflammation and diabetes, inflammatory bowel disease, kidney inflammation and restenosis. Prior art inhibition of VLA-ACS-1 interaction either involves the use of anti-VLA-4 antibodies, which can themselves induce an immune response on repeated administration, or the 25-mer CS-1 peptide, which is large and costly to make and is subject to rapid proteolytic degradation. The peptidominatios of the invention are smaller in comparison to the CS-1 peptide and therefore less expensive to manufacture, and are resistent to proteolytis. Sequences AA777411-Y77414 and AA777434-Y77444 represent fragments of the CS-1 peptide for their ability to inhibit VLA-4 Jurkat cells to immobilised CS-1 peptide
                                                                           The invention relates to peptidomimetic compounds (AAY77415-Y77438) capable of inhibiting the binding of the VLA-4 integrin (alpha-4-beta-1, CD494/CD29) to the CS-1 portion (2S amino acids) of a splice variant of the extracellular matrix protein fibromectin (FN). VLA-4 is expressed on the surface of leukocytes; the CS-1 FN/VLA-4 interaction plays an important role in the maturation and trafficking. VLA-4-mediated leukocyte adhesion to the CS-1 FN of endochelial cells is also a critical step in the inflammatory response. The peptidomimetics of the invention may be used to treat both chronic and acute immunoinflammatory conditions, such as asthma, rheumatoid arthritis, osteoarthritis and allograft rejection. They may also be used to treat psoriasis and other skin inflammations, demyelinating diseases of the central nervous system
New peptidomimetic compounds used as cell surface fibronectin expressing receptor and VLA-4 inhibitors for treating inflammatory and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LDV peptide; VLA-4 inhibitor; very late antigen; alpha-4-beta-1; CD49d/CD29; cell adhesion; arylalkyl azolylalkanoic acid derivative; arylureidoalkyl azolylalkanoic acid derivative; inflammatory disorder; autoimmune disorder; respiratory disorder; LDV motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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100.0%; Pred. No. 7.8e+05;
iive 0; Mismatches 0;
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                                                      Disclosure; Fig 2; 243pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY69619 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VLA-4 inhibitor peptide #2
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                           cardiovascular disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                              5 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                    (AAY77410).
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                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence
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The invention relates to novel arylalkyl and arylureidoalkyl azolylalkanoic acid derivatives and related compounds (1), and their salls and prodrugs. These are are integrin inhibitors, specifically of salts and prodrugs. These are are integrin inhibitors, specifically of VLA-4 (very late annigen 4, also known as alpha 4-beta-1 or CD4943(D29), which mediate cell adhesion. VLA-4 is a receptor for the cytokine-inducible cell surface protein VCAM-1 (vascular cell adhesion molecule-1) and for the alternatively spliced forms of fibronectin (FN) which contain the CS-1 domain. The novel compounds inhibit cell adhesion, and consequent or associated pathogenic processes mediated by VLA-4, and man their caspiratory disorders. These include asthma, arthritis, sutchimmatory bowel disease. Sequences AAY86918-Y695co represent peptides derived from the VLA-4-binding domain of the FN CS-1 region which contain the LDV motif and are known to inhibit fibronectin-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypertenaive nephrosclerosis, hypertensive glomerulosclerosis,
chronic glomerulonephritis, hereditary nephritis, renal dysplasia,
nephrotropic, cell adhesion inhibition, fibronectin CS-1 region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treating a mammal in, or at a risk of developing, chronic renal failure, involves administering at least one integrin antagonist
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 23; DB 21; Pred. No. 7.8e+05; 0; Mismatches 0;
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(UNLO ) IMPERIAL COLLEGE SCI TECHNOLOGY & MED.
Disclosure; Page 2; 120pp; English
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Similarity 100.0%;
5; Conservative 0;
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Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cell adhesion.
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us-09-251-073a-16.closed.rag

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The invention relates to a method for treating a mammal with, or at risk of developing, chronic renal failure, involving the administration of at least one integrin antegonist. The integrin antagonists that may be used in the method include antagonists of alpha-4-subunit containing integrins or antagonists of alpha-1-subunit containing integrins or antagonists of alpha-1-subunit containing integrins. In particular, the antagonists of alpha-1-subunit containing integrins. In particular, the antagonists of alpha-1-subunit integrin and its cognate ligand (collagen IV, and laminin in the case of VLA-1, and fibronectin and VCAV-1 in the case of VLA-4). The method of the invention may be used to treat chronic renal failure, and etage renal disease, chronic diabetic nephropathy, diabetic nephrosts, objections of the case of VLA-1, and fibronectin and VCAV-1 in the case of VLA-4). The method of the invention may be used to treat chronic renal failure, and etage renal dispetic renal hypertrophy, hypertensive nephrosts, chronic diabetic nephrogathy, diabetic renal hypertrophy, hypertensive glomerulosclerosis, chronic glomerulonephritis, hereditary nephritis or renal dysplasia. Sequences AAB73466.AAB73466 represent fibronectin, which inhibit fibronectin-dependent cell adhesion, and may therefore be used in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fibronectin fragment and fibrin related peptide SEQ ID NO:1142.
                                                                                                                                                                                                                                                                                                                                                                        Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thibaudeau
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                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 23; DB 22;
100.0%; Pred. No. 7.8e+05;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bridon DP, Ezrin AM, Milner PG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB91966 standard; Peptide; 5 AA.
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99US-0153406.
99US-0159783.
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                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 5; Conserv
                                                                                                                                                                                                                                                                                                                                    5 AA;
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10-SEP-1999;
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The present invention describes a modified therapeutic peptide (1) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently

Disclosure; Page 569; 733pp; English.

Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity

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bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. It] are useful for modifying therapeutic peptidas e.g. hormonase, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half iffe) and specificity as bonding to large molecules decreases and intracellular uptake and interference with physiological processes AABB0829 to AABB2441 represent peptides which can be used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polypeptides useful in construction of structural models for identifying therapeutic compounds, comprises series of heptad repeats that mimic a transmembrane domain and cytoplasmic domain attached to
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Integrin; transmembrane protein; alpha4 integrin inhibitor; paxillin; immunosuppressive; inflammatory bowel disease; arthritis; multiple sclerosis; asthma; atherosclerosis; wound healing.
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                                                                                                                                                                                                                                                                                                                            Length 5;
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                                                                                                                                                                                                                                                                                                                          100.0%; Score 23; DB 22; 100.0%; Pred. No. 7.8e+05;
                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Integrin recognition peptide sequence #3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB50876 standard; peptide; 5 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2000; 2000WO-US15153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SCRI ) SCRIPPS RES INST.
                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                       5 AA;
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                                                                                                                                                                                                                                                                                       Sequence
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AAB50876
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responses by contacting the structural model with paxillin or a paxillin related molecule in the presence and absence of a test agent and determining binding of paxillin or paxillin related molecule to the structural model. A decrease in binding in the presence of the test agent indicates that the test agent is an inhibitor of alpha4 integrin biological response. Inhibitors of the binding of paxillin to alpha4 are useful in blocking immune responses in conditions such as inflammatory bowel disease, arthritis, multiple sclerosis and asthma and in inhibiting atherosclerosis and scarring during wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polypeptides useful in construction of structural models for identifying therapeutic compounds, comprises series of heptad repeats that mimic a transmembrane domain and cytoplasmic domain attached to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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1es 5; Conservative
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Length 5;

Score 23; DB 22; Pred, No. 7.8e+05;

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Query Match Best Local Similarity

thrombosis and malignancy.

5 AA;

Sequence

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Gaps
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Job time: 33 secs
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Sequence 3, Appli
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(without alignments)
10.077 Million cell updates/sec
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| Patent No. US20020159998A1
| GENERAL INFORMATION:
| APPLICANT: MUNDY, GREGORY R.
| APPLICANT: YONEDA, TOSHIYUKI
| TITLE OF INVENTION: METHODS OF TREATING MULTIPLE MYELOWA AND
| TITLE OF INVENTION: MYELOMA-INDUCED BONE RESORPTION USING INTEGRIN
| FILE REFERENCE: A061CIP2
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1: /cgn2_6/ptodata/2/pubpaa/USO8 NEW PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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/cgnZ_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 US-10-086-217-6
9 US-09-320-907B-3
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Listing first 100 summaries
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                                                                                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Score Match Length DB ID
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23
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US-10-086-217-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: GINSBERG, MARK H.
APPLICANT: GINSBERG, MARK H.
APPLICANT: GINSBERG, MARTIN
TITLE OF INVENTION: STRUCTURAL MODELS FOR CYTOPLASMIC DOMAINS OF
TITLE OF INVENTION: TRANSMEMBRANE RECEPTORS
FILE REFERENCE: STR.0006
CURRENT APPLICATION NUMBER: US/09/320,907B
CURRENT FILING DATE: 1999-05-27
PRIOR APPLICATION NUMBER: 09/187,236
PRIOR PILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: 9260 ID NOS: 25
SEQ ID NO 3
LENGTH: 5
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US-10-086-217-6
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Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels
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CURRENT FILING DATE: 2002-06-21
PRIOR FILING DATE: 2010-08-31
PRIOR FILING DATE: 2010-08-31
PRIOR FILING DATE: 2010-03-13
PRIOR FILING DATE: 2010-03-13
PRIOR APPLICATION NUMBER: PCT/US99/21170
PRIOR APPLICATION NUMBER: PCT/US99/21170
PRIOR APPLICATION NUMBER: 60/100,182
PRIOR PILING DATE: 1998-09-13
PRIOR PILING DATE: 1998-09-14
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATCHTIN VET: 2.1
SEQ ID NO 6
LENGTH: 5
TYPE: PRT

ORGANISM: Artificial Sequence
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Matches 5; Conservative
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US-09-320-907B-3
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Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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Length 5;
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ZUP: 2
STREET: 805 Fifteenth Street, N.W., #700 CITY: Washington
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SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acidd
STRANDEDNESS: single
TOPOLLGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL:
FRAGMENT TYPE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORIGINAL SOURCE:
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PUBLICATION INFORMATION:
AUTHORS:
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IDENTIFICATION METHOD:
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DEVELOPMENTAL STAGE:
HARLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL TINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
POMILE:
UNITS:
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Best Local Similarity
                                                                                       STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN:
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                                                                                                                                                                                                                                                                                  February 8, 2003, 10:28:33 ; Search time 14 Seconds (without alignments) 10.508 Million cell updates/sec
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Sequence 3,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3
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/cgn2 6/ptodata1/iaa/5A_COMB.pep:*
/cgn2 6/ptodata1/iaa/5B_COMB.pep:*
/cgn2 6/ptodata1/iaa/6A_COMB.pep:*
/cgn2 6/ptodata1/iaa/6B_COMB.pep:*
/cgn2 6/ptodata1/iaa/RGTUS_COMB.pep:*
/cgn2 6/ptodata1/iaa/PCTUS_COMB.pep:*
/cgn2 6/ptodata1/iaa/PCTUS_COMB.pep:*
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                                           GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-303-162A-3
US-08-634-060-3
US-08-38-282-10
US-08-709-515-3
US-08-709-846-2
US-09-146-203-3
US-08-983-391-2
US-08-983-372-2
US-08-376-372-2
US-08-375-321-2
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Patent No. 5475100
GENERAL INFORMATION:
APPLICANT: Kimikazu HASHINO et al.
TITLE OF INVENTION: Artificial Antibody
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 100 summaries
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Match Length
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100.0 100.0

Score

Result

100.0

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US-08-109-106-3

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E: Leydig, Voit & Mayer, Ltd.
Two Prudential Plaza, Suite 4900
                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/303,162
FILING DATE: 08-SEP-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kilyk, John Jr.
REGISTRATION NUMBER: 30/63
REFERENCE/DOCKET NUMBER: 71602
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEPHONE: (312) 616-5600
TELEPHONE: (312) 616-500
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                               ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/814,873
FILING DATE: December 24, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/402,389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                      Illinois
: USA
                        STREET: TWO FA
   ADDRESSEE:
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US-08-338-282-10
                                                                                                                                         COUNTRY:
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   Gaps
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Sequence 3, Application US/08634060
Patent No. 5712136
GENERAL INFORMATION:
APPLICANT: Wickham, Thomas J.
APPLICANT: Koveedi, Imre
APPLICANT: Roelvink, Petrus W.
ITLE OF INVENTION: THE ADENOVIRAL-MEDIATED CELL TARGETING COMMANDED BY TITLE OF INVENTION: THE ADENOVIRAL MEDIATED RESE PROTEIN
ITLE OF INVENTION: THE ADENOVIRAL MEDIATED CELL TARGETING COMMANDED BY CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
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   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Kovesdi, Imre
APPLICANT: Brough, Douglas E.
APPLICANT: McVey, Duncan L.
TITLE OF INVENTION: CHIMERIC PENTON BASE MOLECULES
TITLE OF INVENTION: AND METHODS OF USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,162A
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION PARTICULAR DESCRIPTION S14
CLASSIFICATION: S14
ATTORNEY/AGENT INFORMATION:
NAME: Kilyk, John Jr.
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 61306
TELECOMMUNICATION INFORMATION:
THE PERFORMATION:
THE PERFORMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08303162A
Patent No. 555909
GENERAL INFORMATION:
APPLICANT: Wickham, Thomas J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (312) 616-5700
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
5, Conservative
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Vc
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Best Local Similarity
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STRANDEDNESS: sin
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Matches
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Sequence 10, Application US/08338282
Patent No. 5730978
GENERAL INFORMATION:
APPLICANT: WAYNER. B.A.
TITLE OF INVENTION: INHIBITION OF LYMPHOCYTE ADHERENCE TO VASCULAR ENDOTHELIUM NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christeensen, O'Connor, Johnson and Kindness
STREET: 2800 Pacific First Center, 1420 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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STATE: Washington
COUNTRY: Bashington
COUNTRY: Ballol-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage
COMPUTER: IBM PC/386 Compatible
COMPUTER: IBM PC/386 Compatible
OPERATING SYSTEM: MS-DOS 4.01
SOFTWARE: Word for Windows-t
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338,282
SOFTWARE: Patentin Releage #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/634,060
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Gaps
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Patent No. 5962311
GENERAL INFORMATION:
APPLICANT: WICKHAM, THOMAS J.
APPLICANT: ROBLVINK, PETRUS W.
APPLICANT: ROYDEDI, IMRE
TITLE OF INVENTION: A SHORT-SHAFTED ADENOVIRAL FIBER AND ITS
TITLE OF INVENTION: USE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESSE: LEYDIG, VOIT & MAYER, LTD.
STREET: TWO PRUDENTIAL PLAZA, SUITE 4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 5;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,846
FILING DATE: 21-AUG-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: LARCHER, CAROL
REGISTRATION NUMBER: 35243
REGISTRATION NUMBER: 35243
REGISTRATION NUMBER: 36243
REGISTRATION NUMBER: 36243
REGISTRATION NUMBER: 36243
REGISTRATION NUMBER: 31243
RELEPANCE/CONCET UNBER: 74294
TELEPHONE: (312) 616-5000
TELEPHONE: (312) 616-5000
TELEPHONE: (312) 616-5700
SEQUENCE CHARACTERISTICS:
                                                    100.0%; Score 23; DB 1; 1
100.0%; Pred. No. 1.9e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 23; DB 2; 1
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0;
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APPLICANT: Jeffrey W. Smith
APPLICANT: Dana D. Hu
ATTLE OF INVENTION: Integrin Ligand Dissociators
FILE REFERENCE: 02046.0002
CURRENT APPLICATION NUMBER: US/09/146,503
                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 60601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/09146503
Patent No. 6184206
                            Query Match
Best Local Similarity 100.v
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: TWO FIND
                                                                                                                                          1 EILDV 5
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                                                                                                                                                                                                                                                           RESULT 6
US-08-700-846-2
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       US-08-709-515-3
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FILING DATE: September 1, 1989
ATTORNEY/AGENT INFORMATION:
NAME: Sundamo,John,S.
REGISTRATION NUMBER: 34,446
REFERENCE/DOCKET NUMBER: CYTE-1-6162
TELECPMUNICATION INFORMATION:
TELEPHONE: 1-206-682-8100; 1-206-224-0727 (direct)
TELEPAX: 1-206-224-0779
TELEEX: 4938023
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08709515
Patent No. 5731190
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wickham, Thomas J.
APPLICANT: Moveddi, Imre
APPLICANT: Brough, Douglas B.
APPLICANT: Bruder, Joseph T.
TITLE OF INVENTION: CHIMERIC PENTON BASE MOLECULES
TITLE OF INVENTION: CHIMERIC PENTON BASE MOLECULES
TITLE OF INVENTION: AND METHODS OF USING SAME
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSER: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,515
FILING DATE:
CLASSIPLCATION: 514
PRICA APPLICATION DATA:
APPLICATION NUMBER: 08/303,162
FILING DATE: 08-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kilyk, John Jr.
REGISTRATION NUMBER: 30763
REGISTRATION NUMBER: 30763
REGISTRATION NUMBER: 3126
FILEFRAM: (312) 616-5600
TELEFRAM: (312) 616-5700
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARRACTERISTICS:
LENGTH: 5 amino acids
LYNE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.(
Matches 5; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: BILDV
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MOLECULE TYPE: protein
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ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ANTI-SENSE: NO
US-08-498-237-2
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US-08-376-372-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Synthetically generated protein US-08-983-391-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Adams, Steven P.
APPLICANT: Adams, Steven P.
APPLICANT: Caetro, Alfredo C.
APPLICANT: Caetro, Alfredo C.
APPLICANT: Caetwo, Julio Herman
APPLICANT: Cuervo, Julio Herman
APPLICANT: Lee, Wen-Cherng
APPLICANT: Lee, Wen-Cherng
APPLICANT: Almquist, Ronald G.
APPLICANT: Almquist, Roll Betto
CURRENT APPLICATION NUMBER: US/08/983,391
CURRENT PILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: US 96/11570
PRIOR APPLICATION NUMBER: US 96/11570
PRIOR APPLICATION NUMBER: US 08/498,237
PRIOR FILING DATE: 1995-07-11
PRIOR APPLICATION NUMBER: US 08/498,237
PRIOR FILING DATE: 1995-07-11
IRMGTH: S.
ILENGTH: S.
CURRENT FILING DATE: 1998-09-02
BARLIER APPLICATION NUMBER: 60/057,463
EARLIER FILING DATE: 1997-09-03
NUMBER OF SEQ ID NOS: 3
SOFTHARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 5
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Patent No. 6248713
GENERAL INFORMATION:
APPLICANT: Lin, Ko-Chung
APPLICANT: Adams, Steven P
APPLICANT: Adams, Steven P
APPLICANT: Castro, Alfredo C
APPLICANT: Zimmerman, Craig N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08983391
Patent No. 6239108
GENERAL INFORMATION:
                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                            ; OTHER INFORMATION: Synthetic US-09-146-503-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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APPLICANT: Lee, Men-Cherrig
APPLICANT: Lee, Men-Cherrig
APPLICANT: Lee, Men-Cherrig
APPLICANT: CHATCH, MANY BE
APPLICANT: Administ Ronald CHATCH
APPLICANT: New York
CONTRY: New York
APPLICANT: Was York
APPLICANT: Was York
APPLICANT: New York
CONTRY: New York
APPLICANT: Admess Steven P
APPLIC
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1 BILDV 5
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                                  PCT-US95-07542-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.9e+05;
hes ' 0; Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/372
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B180
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELECOMMUNICATION OF 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
OTHER INFORMATION: Synthetically generated peptide
US-08-875-321-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Adams, Steven P.
APPLICANT: Lin, Ko-Chung
APPLICANT: Lin, Ko-Chung
APPLICANT: Lin, Ko-Chung
APPLICANT: Zimmerman, Craig N.
APPLICANT: Ammond, Charles E.
APPLICANT: Histo, Yu-Sheng
APPLICANT: Cuercy, Julio Hernan
APPLICANT: Cuercy, Julio Hernan
APPLICANT: Singh, Juswinder
ITLE OF INVENTION: CELL ADHESION INHIBITORS
FILE REFERENCE: 10274-023002
CURRENT APPLICATION WUMBER: US/08/875,321
CURRENT PILING DATE: 1997-09-27
PRIOR FILING DATE: 1995-01-23
NUMBER OF SEQ ID NOS: 5
SEQ ID NO 2
LENGTH: 5
LENGTH: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08875321
Patent No. 6376538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
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MOLECULE TYPE: peptide
HYPOTHETICAL: NO
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Best Local Similarity
Matches 5; Conserva
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RESULT 12

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Sequence 3. Application PC/TUS9507542

GENERAL INFORMATION:
STRUCTURAL MODELS FOR CYTOPLASMIC
TITLE OF INVENTION: STRUCTURAL MODELS FOR CYTOPLASMIC
TITLE OF INVENTION: DUMAINS OF TRANSMEMBRANE RECEPTORS
NUMBERS OF SEQUENCES:
COMMUTER REDABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBP PC Compacible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PAPELICATION DATA:
APPLICATION NUMBER: PCT/US95/07542
FILING DATE: 13-JUN-1995
FILING DATE: 15-JUN-1995
FILING DATE: 15-JUN-1995
FILING DATE: 15-JUN-1994
FILING DATE: 100.000, Force 23; DB 5; Length 5; DB 5; Length 5; DB 1 BILDV 5

ON 1 BILDV 5

DD 1 BILDV 5

Séarch completed: February 8, 2003, 10:30:42
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H70188 C552649 C55261 A95300 H90388 C66995 C86995 C1402 S01402 T21185 G81905	7870383 7871157 7895182 798182 798182 7986182 79861 79861 79861 7873998 7873998 7873998 7873998 78739999 786054 780958 780958	873751 169485 170323 1704821 1704821 1704821 170543 170554 1725577 1725577 1725577 1725577 1725577 1725577 1725749 172152
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Local Similarity
hes 5; Conserv
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A; Residues: 1-107 < KUN>
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C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Accession: C72047
R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
Aritle: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606; PMID:10192388
A;Reference number: A72000; MUID:99206606; PMID:10192388
A;Residues: Dralminary
A;Residues: 1-50 cARN>
A;Residues: 1-50 cARN>
A;Cross-references: GB:AE001651; GB:AE001363; NID:94376985; PIDN:AAD18824.1; PID:9437698
C;Genetics:
A;Gene: CPn0685
                                                                                                                             hypothetical protein CPj0685 [imported] - Chlamydophila pneumoniae (strain J138)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C;Accession: B86576
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
Mucleic Acids Res 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
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S13787
Conserved hypothetical protein yaak - Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Accession: S13787; S66050; C69737
R;Alonso, J.C.; Shirahige, K.; Ogasawara, N.
Nucleic Acids Res. 18, 6771-6777, 1990
A;Title: Molecular cloning, genetic characterization and DNA sequence analysis of the 1A;Reference number: S13786; MUID:91088245; PMID:2124672
A;Accession: S13787
A;Status: preliminary
A;Residues: 1-107 <ALO>
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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-50 <STO>
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R;Ogasawara, N.; Nakai, S.; Yoshikawa, H.
Dank Res. 1, 1.14, 1994
A;Title: Systematic sequencing of the 180 kilobase region of the Bacillus subtilis chrom A;Reference number: S65967; MUID:96051385; PMID:7584024
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A;Runst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Carter, C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler, iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A;Authors: Lauber, J.; Lazaravic, V.; Berk, S.H.; Bevine, A.; Liu, H.; Masuda, S.; Maueel, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A;Authors: Schleich, S.; Chrocter, R.; Scoffone, F.; Sekfucchi, J.; Sekowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetrara, P.; Toganoi, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Ajttle: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Accession C69737
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C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Daces: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Daces: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Daces: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Acces: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Acces: 10-Sep-1999 #sequence 10-Sep-1999 #text_change 21-Jul-2000
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A;Experimental source: strain 168
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A;Cross-references: EMBL:X17014; NID:g453238; PIDN:CAA34878.1; PID:g40073
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hypothetical protein Vng1169c (imported) - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 0.2 Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Accession: F8472
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablc Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A;Reference number: A84160; MUID:20504483; PMID:11016950
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kinesin heavy chain homolog KIFS - mouse (fragment)
C;5pecies: Mus muscallus (house mouse)
C;5pecies: Mus muscallus (house mouse)
C;5pecies: Muscallus (house mouse)
C;Accesion: C44259
R;Aizawa, H; Sekine, Y; Takemura, R:; Zhang, Z:; Nangaku, M.; Hirokawa, N. J. Cell Biol. 119, 1287-1296, 1992
A;Title: Kinesin family in murine central nervous system.
A;Reference number: A44259; MUID:93077686; PMID:1447303
A;Accession: C44259
A;Residues: preliminary; not compared with conceptual translation
A;Residues: 1-143 <AIZ>
A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIP:118906)
C;Superfamily: kinesin heavy chain; kinesin motor domain homology
F;1-143/Domain: kinesin motor domain homology (fragment)
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A;Molecule type: DNA
A;Redidues: 1-119 <STO>
A;Cross-references: GB:AE004437; NID:g10580704; PIDN:AAG19546.1; GSPDB:GN00138
C;Genetics:
A;Gene: VNG1169C
C;Superfamily: conserved hypothetical protein MJ0039
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probable PTS enzyme II B component [imported] - Bscherichia coli (strain O157:H7, substracy Species: Escherichia coli (c) Peter (c) Pate: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
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A;Molecule type: DNA
A;Residues: 1-146 <STO>
A;Cross-references: GB:AE005174; NID:g12512844; PIDN:AAG54433.1; GSPDB:GN00145; UWGP:Z01/
A;Experimental source: strain O157:H7, substrain BDL933
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R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew Iller, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, B.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
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A;Experimental source: strain H37Rv
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A.Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-146 «HMY»
A;Cross-references: GB:BA000007; PIDN:BAB33556.1; PID:g13359589; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: EC80133
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Cibate: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
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C;Superfamily: Streptomyces coelicolor hypothetical protein SC6G10.02c
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Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                             Length 146;
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C;Accession: AH0568

R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: AB0502; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Genetics:
A;Gene: STY0582
C;Superfamily: phosphoribosylaminoimidazole carboxylase catalytic chain; phosphoribosyla:
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C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 19-Feb-1994 #sequence_revision 23-Feb-1996 #text_change 21-Jul-2000
C;Accession: S24397; S08120
R;Livak, K.J.
Genetics 124, 303-316, 1990
A;Fille: Drosophila melanogaster Stellate genes and their trans A;Reference number: S24397; MUID:90169476; PMID:1689686
A;Accession: S24397
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C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Accession: S24398
R;Livak, K.J.
Genetics 124, 303-316, 1990
A;Title: Detailed structure of the Drosophila melanogaster Stellate genes and their tran.
A;Reference number: S24397; MUD:90169476; PMID:1689686
A;Accession: S24399
A;Molecule type: Drosophila melanogaster Stellate genes and their tran.
A;Andecule type: Drosophila minary
A;Andecule type: Drosophila melanogaster Stellate genes and their tran.
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A;Cross-references: GB:AL513382; PIDN:CAD05018.1; PID:g16501801; GSPDB:GN00176
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A;Reaidues: 1-172 <LIV>
A;Cross-references: EMBL:X15899; NID:g8660; PIDN:CAA33906.1; PID:g295755
C;Genetics:
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Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0;
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100.0%; Score 23; DB 2; L
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0;
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ilarity 100.0%; Pred. No. 2.3e+02;
Conservative 0; Mismatches 0;
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A;Introns: 4/2; 171/2
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                                                                                                                                                                                                                                                                                                                            probable exported protein STY2351 [imported] - Salmonella enterica subsp. enterica serova Typhi
A;Note: this species has also been called Salmonella typhi
C;Species: Salmonella enterica subsp. enterica serovar Typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C;Accession: AG0772
A;Reference number: AB0502; PMID:11677608
A;Reference number: AB0502; PMID:11677608
A;Retus: preliminary
A;Molecule type: DNA
A;Retus: preliminary
A;Molecule type: DNA
A;Cross-references: GB:AL513382; PIDN:CAD02501.1; PID:g16503365; GSPDB:GN00176
C;Genetics:
A;Genetics:
A;Genet
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AH0568
Phosphoribosylaminoimidazole carboxylase catalytic chain [imported] - Salmon Phosphoribosylaminoimidazole carboxylase catalytic chain [imported] - Salmon C; Species: Salmonella enterica subsp. enterica serovar Typhi A; Note: this species has also been called Salmonella typhi C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
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A;Gene: greA, UU304
C;Genetic code: SGC3
C;Superfanily: transcription elongation factor greb
C;Keywords: transcription factor
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rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
A.Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Praser, C.M.; Smith, H.O.; Woese, C A.Artile: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii A.Freference number: A64300; MUID:96337999; PMID:8688087
A.Accession: A64431
A.Status: preliminary; nucleic acid sequence not shown; translation not shown A.Molecule type: DNA
A.Residues: 1-177 <BUL>
                                                                                                                                                                                                                                                         A; Cross-references: GB:U67548; GB:L77117; NID:g2826361; PIDN:AAB99053.1; PID:g1499895; T1
C; Genetics:
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R; Tettelin, H.; Nelson, K.E.; Pauleen, I.T.; Elsen, J.A.; Read, T.D.; Peterson, S.; Heidt on, J.D.; Udayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, I nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumonlae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:AE005672; PIDN:AAK75384.1; PID:g14972764; GSPDB:GN00164; TIGR:SP46
A;Experimental source: strain TIGR4
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cjaccession: E98016
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; E
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; E
R;Hoskins, D.A.; Alborn Jr., W.; Lefkowitz, E.J.; Lu, J.; Mateushima, P.; McAhren, S.; M
y, R.; Sun, P.M.; Winkler, M.E.
A; Bacteriol. 183, 5709-5717, 2001
A;Authors; Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    conserved hypothetical protein SP1280 [imported] - Streptococcus pneumoniae (strain TIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      conserved hypothetical protein spr1158 [imported] - Streptococcus pneumoniae (strain R6)
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A;Gross-references: GB:AE007317; PIDN:AAK99961.1; PID:g15458788; GSPDB:GN00174
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
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C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 180;
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100.0%; Pred. No. 2.4e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                               A,Map position: FOR987440-987973
C;Superfamily: conserved hypothetical protein MJ1050
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 5; Conserv
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A.Molecule type: DNA
A.Residues: 1-180 <KUR>
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A, Status: preliminary
A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 EILDV 122
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Best Local S:
Matches 5
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197114

Uncharacterized conserved protein (coiled-coil) CAC1739 [imported] - Clostridium acetobu uncharacterized conserved protein (coiled-coil) CAC1739 [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C;Accession: P97114

R;Nolling, J; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Bacteriol. 183, 4823-4838, 2001

A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc A;Reference number: A96900; MUD:21359325; PMID:21359325

A;Accession: F97114

A;Residues: preliminary

A;Molecule type: DNA

A;Residues: 1-174 «KUR»

A;Residues: 1-174 «KUR»

A;Cross-references: GB:AE001437; PIDN:AAK79705.1; PID:G15024707; GSPDB:GN00168

A;Sepecies: Coortidium acetobutylicum ATCC824

C;Genetics:
A;Gene: CAC1739
                                                                                                                                                                                                            All Species: Versinia pestis
C.Species: Versinia pestis
R.Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
R.Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, R.W.; Davis, P.; Dougan, G.;
Nature 413, 323-527, 2001
A.Reference number: AB0001; MUID:21470413; PMID:11586360
A.Reference number: AB0001; MUID:21470413; PMID:11586360
A.Stetuus: preliminary
A.Stetuus: Preliminary
A.Stetuus: C.S.M.R.A.Species: GB:AL590842; PIDN:CAC92450.1; PID:g15981151; GSPDB:GN00175
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hypothetical protein MJ1050 - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Decies: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: A64431
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R;Bult, C.J.; Overbeek, R.; Kirkness, B.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Genetics:
A;Gene: aroL
C;Superfamily: shikimate kinase; shikimate kinase homology
C;Keywords: phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 23; DB 2; I 100.0%; Pred. No. 2.3e+02;
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Matches 5; Conservative
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Best Local Similarity
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            EILDV
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Gaps

Query Match

Matches

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C,Accession: A03484
R;Torok, 1.; Kondorosi, B.; Stepkowski, T.; Posfai, J.; Kondorosi, A.
Nucleic Acids Res. 12, 9509-9524, 1984
A;Title: Nucleotide sequence of Rhizobium meliloti nodulation genes.
A;Reference number: A93553; MUD:85087953; PMID:6336331
A;Accession 033484
A;Molecule type: DNA
A;Residues: 1-217 <TOR>
A;Cross references: GB:X01649; GB:M13287; NID:946287; PIDN:CAA25809.1; PID:946290
A;Experimental source: strain 41
C;Comment: This is one of the proteins, coded by nodulation genes, that are required for C;Genetics:
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C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: B95321
R;Barnett, M.G.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowse
F.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.,
F. Xalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.,
F. Xalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.,
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilots
A;Reference number: A95262; MUID:21396509; PMID:11481432
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A, Accession: B95321
A, Accession: B95321
A, Accession: B95321
A, Status: preliminary
A, Status: preliminary
A, Molecule type: DNA
A, Status: preliminary
A, Molecule type: DNA
A, Status: DNA
A, Cross references: GB: EE006469; PIDN: AAK65132.1; PID: g14523571; GSPDB: GN00165
A, Experimental source: strain 1021, megaplasmid pSyma
A, Cross references: GB: EE006469; PIDN: AAK65132.1; PID: g14523571; GSPDB: GN00165
A, Experimental source: strain 1021, megaplasmid pSyma
R; Gallbert, F.; Finna, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A, Authoris: Kahn, D.; Kahn, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C.
A, Attle: The composite genome of the legume symbiont Sinorhizobium meliloti.
A, Reference number: A96039; MUID: 21368234; PMID: 11474104
A; Contents: annotation
C, Genetics:
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nodulation protein nodB - Rhizobium meliloti (strain 41)
C;Species: Rhizobium meliloti
C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 16-Jul-1999
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C,Species: Thermotoga maritima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 23; DB 1; Length 217; Best Local Similarity 100.0%; Pred. No. 2.9e+02; Matches 5; Conservative 0; Mismatches 0; Indels
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A;Genome: plasmid
C;Superfamily: nodulation protein nodB; nodB homology
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Matches 5; Conserv
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ZZZRBM
nodulation protein nodB - Rhizobium meliloti
C;Species: Rhizobium meliloti
C;Species: Rhizobium meliloti
C;Species: Rhizobium meliloti
C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 11-Apr-1997
C;Accession: A03483
R;Egelhoff, T.T.; Fisher, R.F.; Jacobs, T.W.; Mulligan, J.T.; Long, S.R.
DNA 4, 241-248, 1985
A;Title: Nucleotide sequence of Rhizobium meliloti 1021 nodulation genes: nodD is read of A;Reference number: A90951; MUD:85229955; PMID:4006668
A;Reference number: A90951; MUD:85229955; PMID:4006668
A;Residues: 1-217 <cgraph colored colore
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                                                                                                      100.0%; Score 23; DB 2; Length 180; 100.0%; Pred. No. 2.4e+02;
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                                                                                                                                                                                                             0; Mismatches
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Matches 5; Conserva
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EILDV 37
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A, Introns: 132/1
A, Note: T4C9.40
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          A;Gene: spr1158
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Query Match

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174 EILDV 178
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Cispecies: Agrobacterium tumefaciens
Cispecies: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
Ciscession: B98297
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2322-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; PMID:11743194
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A.Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AE001708, GB:AE000512; NID:g4980740; PIDN:AAD35348.1; PID:g498075
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM0260
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: C72400
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                        Nature 399, 323-329, 1999
Affile: Svidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Atlete Svidence for lateral gene transfer pMID:10360571
A;Accession: C72400
A;Accession: Preliminary
A;Accession: preliminary
A;Accule type: DAN
A;Accule 1-222 <ARN>
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A,Accession: AE2586
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-231 <KUR>
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A;Molecule type: DNA
A;Residues: 1-231 «KUR»
A;Cross-references: GB:AE007870; PIDN:AAK89900.1; PID:g15159849; GSPDB:GN00170
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A,Map positIon: linear chromosome
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Conserved hypothetical protein WTH1192 - Methanobacterium thermoautotrophicum (strain De) Conserved hypothetical protein with thermoautotrophicum (c) Species: Methanobacterium thermoautotrophicum (c) Species: Methanobacterium thermoautotrophicum (c) Species: Methanobacterium thermoautotrophicum (c) Accession: A69026 R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; I c, Mon, J.; Spadafora, R.; Vicaire, R.; Wierzbowski, J.; Gibson, R.; Jiwani, N.; J. Bacteriol. 179, 7135-7155, 1997. Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. A;Thie: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct: A;Accession: A69026 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Nolecule type: DNA A;Residues: 1242 <#MTH>
A;Koss-references: GB:AE000887; GB:AE000666; NID:g2622289; PIDN:AAB85681.1; PID:g2622306 C;Genetics:
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C;Date: 18-701-2001 #sequence_revision 18-701-2001 #text_change 03-Aug-2001
C;Accession: B91020
C;Accession: B91020
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.,
ByA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Bscherichia coli 0157:H7 and genome
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: B91020
A;Status: preliminary
A;Molecule type: DNA
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A;Cross-references: GB:AE008689; PIDN:AAL44307.1; PID:g17741896; GSPDB:GN00187 A;Experimental source: strain C58 (Dupont) C;Genetics: C;Genetics: Atu3494 A;Map position: linear chromosome
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A;Cross-references: GB:BA000007; PIDN:BAB36553.1; PID:g13362600; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
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                                                                                                                                                                                                                                         Length 231;
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Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0;
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Nitrate transport ATP binding protein, probable SMa0581 [imported] - Sinorhizobium melilc C; Species: Sinorhizobium meliloti
C; Species: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 17-May-2002
C; Accession: A95300
R; Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowselly, Ralman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C., Ajtile: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot. A; Reference number: A95262; MUID:21396509; PMID:11481432
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A; Molecule type: DNA
A; Residues: 1-266 < KUR>
A; Cross-references: GB: AED06469; PIDN: AAK64963.1; PID: g14523388; GSPDB: GN00165
A; Cross-references: GB: AED06469; PIDN: AAK64963.1; PID: g14523388; GSPDB: GN00165
A; Experimental source: strain 1021, megaplasmid pSyma
A; Experimental source: strain 1021, megaplasmid pSyma
B; Galibert, F; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, R; Galibert, F; Finan, T.M.; Long, S.R.; Puhler, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
pela, D.; Chain, P.; Gomes, T.
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Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
Abbault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.Cl
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Klebsiella pneumoniae
C;Species: Klebsiella pneumoniae
C;Date: 2.5-Aug-1955 #sequence_revision 25-Aug-1995 #text_change 02-Feb-2001
C;Accession: C55581
R;Lin, J.T.; Goldman, B.S.; Stewart, V.
Bacteriol. 176, 2551-2559, 1994
A;Title: The nasFBDCBA operon for nitrate and nitrite assimilation in Klebsiella pneumon A;Reference number: A55581; MUID:94222832; PMID:8169203
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A,Cross-references: GB:L27431; NID:g1119218; PID:g473439
C,Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology C,Superfamily: nucleotide binding; P-loop F;23-214/Domain: ATP-binding cassette homology <ABC>
F;23-214/Domain: ATP-binding cassette homology <ABC>
F;40-47/Region: nucleotide-binding motif A (P-loop)
                             A;Molecule type: DNA
A;Residues: 1-25 < COES.
A;Cross-references: EMBL:AF038620; FIDN:AAB93487.1; GSPDB:GN00022; CESP:H10D12.2
A;Experimental source: strain Bristol N2; clone H10D12
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A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: DNA
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100.0%; Pred. No. 3.5e+02;
ive 0; Mismatches 0;
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100.0%; Score 23; DB 2; I
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 5; Conservative 0; Mismatches 0;
A; Status: preliminary; translated from GB/EMBL/DDBJ
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Conservative (
                                                                                                                                                          C,Genetics:
A,Gene: CESP:H10D12.2
A,Map position: 4
A;Introns: 25/1; 80/1; 133/1
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Matches 5; Conserv
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() Species: Borrella burgdorferi (Lyme disease spirochete)
() Species: Borrella burgdorferi (Lyme disease spirochete)
() Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999
() Accession: H70188
() R. Fraser, C. M.; Casjens, S.; Huang, M. M.; Sutton, G. G.; Clayton, R.; Lathigra, R.; White Son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, Son, D.; Bowman, C.; Garland, S.; Fuji, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Alathors: Smith, H.O.; Venter, J.C.
(A, Hatch Grount sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
(A, Reference number: A70100; MUID:98055943; PMID:9403685
(A, Reference number: A70100; MUID:98055943; PMID:9403685
(A, Residues: preliminary; nucleic acid sequence not shown; translation not shown
(A, Residues: 1-253 < KLE>
(A, Residues: 1-253 < KLE>
(A, Residues: 1-253 < KLE>
(A, Residues: Legen B.)
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A;Cross-references: GB:AE005174; NID:g12516588; PIDN:AAG57376.1; GSPDB:GN00145; UWGP:Z35
A;Experimental source: strain O157:H7, substrain EDL933
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T32649
R;Ozersky, P.
Rubatted to the EMBL Data Library, December 1997
A;Description: The sequence of C. elegans cosmid H10D12.
A;Reference number: Z21205
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C;Superfamily: 2,4-dihydroxyhept-2-ene-1,7
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Matches 5; Conserv
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   146 EILDV
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regulator of purine blosynthetic genes [imported] - Lactococcus lactis subsp. lactis (st) regulator of purine blosynthetic genes [imported] - Lactococcus lactis subsp. lactis (c) Species: Lactococcus lactis subsp. lactis (c) Species: Lactococcus lactis subsp. lactis (c) Species: Lactococcus lactis subsp. lactis (c) Accession: C86907 (c) Anncker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlic Genome Res. 11, 731-753, 2001 (d) Anncker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlic A; Feference number: A86625; MUD:21235186; PMID:11337471 (accession: C86907) A; Accession: C86907 (annother accession: C86907) A; Accession: L271 csTO> A; Accession: L271 csTO> A; Accession: L271 csTO> A; Accessiones: L271 csTO> A; Accessiones: L271 csTO> A; Accessiones: Selectences: GB. Accession: L271 csTO> A; Accessiones: CB. Accessiones: CB
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R;Ohta, S.; Yohda, M.; Ishizuka, M.; Hirata, H.; Hamamoto, T.; Otawara-Hamamoto, Y.; Mat: B;Ohta, S.; Yohda, M.; Ishizuka, M.; Hirata, Hamamoto, T.; Otawara-Hamamoto, Y.; Mat: A;Othia, B.; Yohda, M.; Ishizuka, M.; 1988
A;Title: Sequence and over-expression of subunits of adenosine triphosphate synthase in tA;Reference number: $01197; MUID:88163679; PMID:2894854
A;Accession: $01402
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A;Note: part of this sequence, including the amino end of the mature protein, was confirm
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C;Species: thermophilic bacterium PS-3
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 03-Jun-2002
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CjSuperfamily: H+-transporting ATP synthase gamma chain
CjKeywords: ATP biosynthesis; hydrolase; membrane-associated complex
FjS-286/Product: H+-transporting ATP synthase gamma chain #status experimental <MAT>
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R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, Science 293, 2093, 2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii. A;Reference number: A97700; MUID:21442074; PMID:11557893
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A, Status: preliminary
A, Molecule type: DNA
A, Molecule: 1-289 KNUR>
A, Residues: 1-289 KNUR>
A, Cross-references: GB: Ab006914; PIDN: AAL03503.1; PID: g15620077; GSPDB: GN00173
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C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 01-Mar-2002
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100.0%; Score 23; DB 2; Length 271;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
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A;Residues: 1-286 <OHT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EILDV 5
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C78peciaes: Bencharichia coli (strain K-12)

C78peciaes: Bencharichia coli

C78peciaes: C64995

C78ccession: C64995

C78cccession: C64995

C78cccssion: C78ccssion: C78ccssion: C78ccssion: C78ccssion: C78ccssion: C78ccssion: C78ccssion: C7
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A, Contents: annotation
C, Genetics:
A, Gene: SMa0581
A, Genome: plasmid
C, Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology
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100.0%; Score 23; DB 2; Length 266;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 1 0; Indels
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C;Superfamily: erythrocyte band 7 integral membrane protein
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100.0%; Score 23; DB 2; L
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 0;
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Best Local Similarity
Matches 5; Conserva
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A;Molecule type: DNA
A;Residues: 1-267 <KUR>
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sulfate adenylyltransferase, chain 2 NMB1192, NMB1154 [imported] - Neisseria meningitidi:
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R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vanathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grand, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ven
A;Hitle: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AE002467; GB:AE002098; NID:g7226426; PIDN:AAF41575.1; PID:g7226429
A;Experimental source: serogroup B, strain MC58
A;Accession: B81115
A;Molecule type: DNA
A;Residues: 1-307 <TE2>
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A;Experimental source: serogroup B, strain MC58
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R;Chamovitz, D.; Misawa, N.; Sandmann, G.; Hirschberg, J.
FEBS Lett. 296, 305-310, 1992
A;Title: Molecular cloning and expression in Escherichia coli of a cyanobacterial gene cola, R;Reference number: $20383; MUID:92164786; PMID:1537409
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probable 608 acidic ribosomal protein p0 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
                                                                                                                                                         C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
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A;Variety: PCC 7942
C;Date: 19-Feb-1994 #sequence_revision 01-Mar-1996 #text_change 02-Mar-2001
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A;Residues: 1-307 <CHA>
A;Cross-references: EMBL:X63873; NID:g46486; PIDN:CAA45350.1; PID:g46487
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Best Local Similarity 100.0%;
Matches 5; Conservative 0
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Best Local Similarity
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A; Residues: 1-307 <TET>
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244 EILDV 248
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general adenylyltransferase (EC 2.7.7.4) chain 2 NWA1365 [imported] - Neisseria probable sulfate adenylyltransferase (EC 2.7.7.4) chain 2 NWA1365 [imported] - Neisseria C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Accession: G81905
R;Parkhill, J; Achtman, M; James, K.D; Bentley, S.D; Churcher, C.; Klee, S.R.; Morel; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Status: preliminary
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A;Residues: 1-307 <PAR>
A;Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84611.1; PID:g738003
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein F21A3.3 - Caenorhabditis elegans closured by checkers. Caenorhabditis elegans closured by a sequence_revision 15-Oct-1999 #text_change 15-Sep-2000 closures. 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Sep-2000 closures. T21185 closured to the EMBL Data Library, November 1996 closure translated to the EMBL Data Library, November 1996 closures. T21185 closures. T21185 closures. T21185 closures. T2186 closures. EMBL:Z81509; PIDN:CAB04157.1; GSPDB:GN00023; CESP:F21A3.3 closures. Closures
                                  A;Gene: ubiG
C;Superfamily: 3-demethylubiquinone-9 3-0-methyltransferase; bioC homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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C;Superfamily: Caenorhabditis elegans hypothetical protein ZC13.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 23; DB 2; Length 290; Best Local Similarity 100.0%; Pred. No. 4.1e+02; Matches 5; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                  Length 289;
                                                                                                                                                         100.0%; Score 23; DB 2; Length 28 llarity 100.0%; Pred. No. 4.1e+02; Conservative 0; Mismatches 0; Indels
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C,Superfamily: nodulation protein nodP
C,Keywords: nucleotidyltransferase
                                                                                                                                                     Query Match
Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                        104 EILDV 108
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C;Genetics
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A;Residues: 1-321 «KUR»
A;Cross-references: GB:AE005672; PIDN:AAK75650.1; PID:g14973054; GSPDB:GN00164; TIGR:SP46
A;Expendental source: strain TIGR4
C;Genetics:
A;Gene: SP1563
C;Superfamily: thioredoxin reductase; thioredoxin reductase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein SA0511 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #text_change 22-Oct-2001
C;Accesion: C9823
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogucl ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thioredoxin-disulfide reductase (EC 1.8.1.9) [imported] - Streptococcus pneumoniae (stra)
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Cipate: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 03-Jun-2002
Cipate: 22-Oct-2001 #sequence_revision 22-Oct-2001
Cipate: 22-Oct-2001 #sequence_revision Jr., Mr., Junoloff, Blasscak, L.; Burgett, S.; DeHoff, B.S.; Bi
Cipate: D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; Mr.
J. Bacteriol. D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; Mr.
A,Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A,Fitle: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A,Reference number: A97872; MUID:21429245; PMID:11544234
A,Accession: D98049
A,Accession: D98049
A,Residues: L-322 < kUR>
A,Residues: L-322 < kUR>
A,Cross-references: GB:AB007317; PIDN:AAL00225.1; PID:g15459075; GSPDB:GN00174
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A;Molecule type: DNA
A;Residues: 1-21 <KUL>
A;Cross-references: GB:BA000018; PID:g13700444; PIDN:BAB41742.1; GSPDB:GN00149
A;Experimental source: strain N315
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C;Superfamily: thioredoxin reductase; thioredoxin reductase homology
C;Keywords: oxidoreductase
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                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 23; DB 2; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0;
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51 EILDV 55
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CiSpeciae: Mycoplasma pneumoniae
NyAlternate names: hypothetical protein D09_orf320
CiSpeciae: Mycoplasma pneumoniae
A, Variety: ATCC 29342
C; Date: 26-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 07-Dec-1999
C; Accession: 873413
R; Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.
Nuclaic Acids Res. 24, 4420-4449, 1996
A; Reterence number: 873327; MUID:97105885; PMID:8948633
A; Reterence number: 873327; MUID:97105885; PMID:8948633
A; Reterence number: 873327; MUID:97105885; PMID:8948633
A; Reterences number: 873413
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Residues: 1-320 «HIM»
A; Resid
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A95182

Pypothetical protein SPI563 [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 01-Feb-2002
C;Accession: A95182
R;Tetelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Accession: A95182
A;Csession: A95182
A;Accession: A95182
A;Molecule type: DNA
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000 C;Accession: T41157 R;Hilbert, H.; Duesterhoeft, A.; Wood, V.; Rajandream, M.A.; Barrell, B.G. Bubmitted to the EMBL Data Library, October 1998 A;Reference number: 221973 A;Accession: T41157 A;Accession: T41157 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Status: preliminary; translated from GB/EMBL/DDBJ A;Residues: DNA A;Residues: 1-312 <HIL>A;Cross-references: EMBL:AL031907; PIDN:CAA21428:1; GSPDB:GN00068; SPDB:SPCC18.14c A;Experimental source: strain 972h-; cosmid c18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Introns: 262/3
C;Superfamily: rat acidic ribosomal protein P0
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Best Local Similarity 100...
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A,Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.A A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: D64665
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Redidues: preliminary; nucleic acid sequence not shown; translation not shown A;Redidues: 1-324 crOM>
A;Redidues: 1-324 crOM>
A;Cross-references: GB:AE000622; GB:AE000511; NID:g2314317; PIDN:AAD08209.1; PID:g2314321
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Riklenk, H.B.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.B.; Ketchum, K.A.; Dodson, Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.P., Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
Alauthors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N. Smith, H.O.; Woese, C.R.; Venter, J.C.
Artile: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon A;Reference number: A69250; MUD: 98049343; PMID: 9389475
A;Accession: D69461
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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A;Toross-referances: GB:AE000986; GB:AE000782; NID:g2689309; PIDN:AAB89555.1; PID:g264886(
C;Superfamily: phosphoribosylformylglycinamidine cyclo-ligase; phosphoribosylformylglycir
F;6-326/Domain: phosphoribosylformylglycinamidine cyclo-ligase homology «PFCL»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein phosphatases ppl regulatory subunit sds22 - fission yeast (Schizosaccharomyces pcl; Species: Schizosaccharomyces pombe C; Species: Schizosaccharomyces pombe C; Date: 13-Jan-1995 #sequence revision 10-Feb-1995 #text_change 26-May-2000 C; Accession: 843988; T38782; A38439 R; Scone, E.M.; Yamano, H.; Kinoshita, N.; Yanagida, M. Curr. Biol. 3, 13-26, 1993 A; Title: Mitotic regulation of protein phosphatases by the fission yeast sds22 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           phosphoribosylformylglycinamidine cyclo-ligase (purM) homolog - Archaeoglobus fulgidus
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A;Experimental source: strain 972h-; cosmid c4A8
R;Ohkura, H.; Yanagida, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C,Species: Archaeoglobus fulgidus
C,Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 16-Jul-1999
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A;Accession: 843988
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-332 <870>
R;Skelton, J; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, submitted to the EMBL Data Library, August 1997
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                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 23; DB 2; Length 324; Best Local Similarity 100.0%; Pred. No. 4.6e+02; Matches 5; Conservative 0; Mismatches 0; Indels
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A;Molecule type: DNA
A;Residues: 1-332 <SKE>
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C71851
probable thioredoxin reductase - Helicobacter pylori (strain J99)
C, Species: Helicobacter pylori
A, Waziety: strain J99
C, Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
C, Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
C, Accession: C71851
R, Alm. R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Inces, C.; Gibson, R.; Marberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.B.; Vovis, G.F.; Nature: 397, 176-180, 1999
A, Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A, Reference number: A71800; MUID: 99120557; PMID: 9923682
A, Accession: C71851
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-324 <ARN>
A, Residues: 1-324 <ARN>
A, Residues: PRESENCE: SEXPONSANOS A, RESPERENCE: SEXPONSANOS B, RESPERE
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C; Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
C; Accession: D64665
R; Tomb, J.F.; White, O; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
                                                                                                                                                                                                                                                                                                                                    C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 07-Dec-1999
C;Accession: T36941
R;Seeger, K.J.; Harris, D.; Thomson, N.R.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, September 1999
A;Reference number: Z21607
A;Accession: T36941
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Residues: 1-322 <SEE>
A;Cross-references: EMBL:AL109962; PIDN:CAB53126.1; GSPDB:GN00070; SCOEDB:SCJ1.08
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SCJ1.08
C;Keywords: transcription initiation
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Matches 5; Conservative
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A; Residues: 1-338 < KAT>
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A; Residues: 1-338 < KAT>
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Conserved hypothetical UU077 [imported] - Ureaplasma urealyticum
Cjspecies Ureaplasma urealyticum
Cjspecies 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
CjAccession: A82937
CjAccession: A82937
Stolass, J.I.; Leffkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
Submitted to GenBank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mir
A;Reference number: A82870
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-313 <GLA>
A;Residues: 1-313 <GLA>
A;Residues: 1-313 <GLA>
A;Cross-references: GB:AE002107; GB:AF222894; NiD:g6899022; PIDN:AAF30482.1; GSPDB:GN001
A;Experimental source: serovar 3; biovar 1
Cell 64, 149-157, 1991
A;Title: Schizosaccharcmyces pombe gene sds22+ essential for a midmitotic transition end A;Atlete: Schizosaccharcmyces pombe gene sds22+ essential for a midmitotic transition end A;Accession: A38439; MUID:91098642; PMID:1846086
A;Accession: A38439
A;Status: preliminary
A;Status: preliminary
A;Residues: 53-332 cOHK>
A;Cross-references: GB:M57495; NID:9173478; PIDN:AAA35342.1; PID:9173479
                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: 1
A;Introns: 41/3
C;Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan
C;Keywords: nucleus
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Best Local Similarity 100.
Matches 5; Conservative
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A;Gene: sds22; SPAC4A8.12c
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A,Gene: UU077
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aspartate-semialdehyde dehydrogenase (EC 1.2.1.11) - Shewanella sp. DSS12
N;Alternate names: aspartate beta-D-semialdehyde dehydrogenase
C;Species: Shewanella sp. DSS12
C;Date: 17-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 20-Jun-2000
C;Accession: JC5436
E;Kato, C.; Smorawinska, M.; Li, L.; Horikoshi, K.
J. Biochem. 121, 717-723, 1997
A;Title: Comparison of the gene expression of aspartate beta-D-semialdehyde dehydrogenasr
A;Reference number: JC5435; MUID:97306055; PMID:9163523
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R;Asto, C.; Smorawinska, M.; Li, L.; Horikoshi, K.
N. Biochem. 121, 717-723, 1997
A;Title: Comparison of the gene expression of aspartate beta-D-semialdehyde dehydrogenas
A;Reference number: JC5435; MUID:97306055; PMID:9163523
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A;Experimental source: strain DSS12
C;Comment: This enzyme is a key enzyme in the biosynthetic pathway of lysine, threonine,
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A;Experimental source: strain DB6705
C;Comment: This enzyme is a key enzyme in the biosynthetic pathway of lysine, threonine,
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; Score 23; DB 2; I
; Pred. No. 4.9e+02;
0; Mismatches 0;
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C;Superfamily: aspartate-semialdehyde dehydrogenase
C;Keywords: oxidoreductase
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C;Superfamily: aspartate-semialdehyde dehydrogenase
C;Keywords: oxidoreductase
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J. Biol. Chem. 263, 12109-12114, 1988
A;Title: Transcriptional Organization of the dnaN and recF Genes of Escherichia coli K-1;
A;Reference number: I41190; MUID:8829898; PMID:2841344
A;Accession: I41190
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A;Title: Overlapping arrangement of the recF and dnaN operons of Escherichia coli, Positi
A;Reference number: IS4000; MUID:86301872; PMID:3527871
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A; Molecule type: DNA
A; Residues: 297-366 < BLA>
A; Cross-references: GB: K02179; NID: g147537; PIDN: AAA24510.1; PID: g147538
R; Adachi, T.; Mizuuchi, K.; Menzel, R.; Gellert, M.
R; Adachi, T.; Mizuuchi, K.; Menzel, R.; Gellert, M.
A; Title: DNA sequence and transcription of the region upstream of the E. coli gyrB gene.
A; Reference number: A22168; MUID: 84297235; PMID: 6089112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA-directed DNA polymerase (EC 2.7.7.7) III beta chain - Bscherichia coli (strain K-12)
   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-357 <GWL
A;Residues: 1-357 <GWL
A;Residues: Efferences: EMBL;AL031603; PIDN:CAA20909.1; GSPDB:GN00068; SPDB:SPCC330.04c
A;Experimental source: strain 972h-; cosmid c330
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,Molecule type: DNA
,Residues: 342-366 <ADA>
,Cross-references: GB:X04341, GB:X00870, NID:g41643; PIDN:CAA27869.1; PID:g41644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Escherichia coli
C;Dace: 28-Aug-1985 #sequence_revision 31-Mar-1988 #text_change 01-Mar-2002
C;Accession: Ap1510; A93996; A22168; I41190; I54000; F65172; A00719; B24944
R;Ohmori, H.; Kimura, M.; Nagata, T.; Sakakibara, Y.
Gene 28, 159-170, 1984
A;Title: Structural analysis of the dnaA and dnaN genes of Escherichia coli.
A;Reference number: A91510; MUID:84237568; PMID:6234204
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A,Accession: A91510
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-366 <OHM>
A,Cross-references: GB:J01602; NID:g145758; PIDN:AAB59150.1; PID:g145761
A,Experimental source: strain K-12
R,Blanar, M.A.; Sandler, S.J.; Armengod, M.E.; Ream, L.W.; Clark, A.J.
Proc. Natl. Acad. Sci. U.S.A. 81, 4622-4626, 1984
A,Title: Molecular analysis of the recF gene of Escherichia coli.
A,Reference number: A93996; MUID:84272685; PMID:6379647
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                                                                                                                                                                                                                                 A;Gene: SPDB:SPCC330.04c
A;Map position: 3
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Best Local Similarity
Matches 5; Conserv
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A;Molecule type: DNA
A;Residues: 1-14 <RES>
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## flagellar motor switch protein (flig-2) homolog - Lywe disease spirochete c; Species: Borrelia burgdorferi (Lywe disease spirochete)

C; Species: Borrelia burgdorferi (Lywe disease spirochete)

C; Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 26-Aug-1999

C; Accession: B70136

R; Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Nature 390, 580-586, 1997

A; Authors: Smith, H.O.; Venter, J.C.

A; Title: Genomic sequence of a Lywe disease spirochaete, Borrelia burgdorferi.

A; Reference number: A70100; MUID:98065943; PMID:9403685

A; Reference number: A70100; MUID:98065943; PMID:9403685

A; Accession: B70136

A; Accession: B70136

A; Residues: L-344 *KLE>

A; Roberts: Parteliainary; nucleic acid sequence not shown; translation not shown
A; Residues: L-344 *KLE>

A; Cross-references: GB:AE001137; GB:AE000783; NID:92688160; PIDN:AAC66658.1; PID:9268817

A; Experimental source: strain B31

C; Superfamily: flagellar switch protein flig
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C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Accession: 323508; S23509
R; Cheetham, M.E.; Brion, J.P.; Anderton, B.H.
B; Cheetham, M.E.; Brion, J.P.; Anderton, B.H.
A; Residues: S23508
A; Status: prellminary
A; Molecule type: mRNA
A; Residues: 1-351
A; Cross-references: BMBL:X63368; NID:g32468; PIDN:CAA44968.1; PID:g32469
A; Status: prellminary
A; Molecule type: mRNA
A; Residues: 1-274, 'DyF' <CH2>
A; Cross-references: BMBL:X63368; NID:g32468; PIDN:CAA44969.1; PID:g32470
C; Genetics:
A; Introns: 275/1
C; Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
F; 3-69/Domain: dnaJ amino-terminal homology <Chapter Species (Signature)
C; Superfamily: heat shock protein dnaJ amino-terminal homology
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T41314
hypothetical repeat-containing protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Bate: 03-19c-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T41314
R;Gwilliam, R; Barrell, B.G.; Rajandream, M.A.; Wedler, H.; Wambutt, R.
submitted to the EMBL Data Library, September 1998
A;Reference number: Z21987
A;Reference number: Z21987
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100.0%; Pred. No. 5e+02;
tive 0; Mismatches 0;
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Best Local Similarity 100.0°
Matches 5; Conservative
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EILDV 12
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Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-366 <KUR>
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D91208
DNA polymerase III beta-subunit [imported] - Escherichia coli (strain O157:H7, substrain C; Species: Escherichia coli
C; Species: Escherichia coli
C; Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C; Accession: D91208
R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gench; A; Reference number: A99629; MUID:21156231; PMID:11258796
A; Reference number: A99629; MUID:21156231; PMID:11258796
A; Residues: preliminary
A; Molecule type: DNA
A; Residues: 1-366 c.HAY>
A; Cross-references: GB:BA000007; PIDN:BAB38059:1; PID:g13364111; GSPDB:GN00154
A; Excerimental source: strain O157:H7, substrain RIMD 0509952
A; Reference number: A64720; MUID:97426617; PMID:9278503
A; Accession: F65172
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-366 *BLAT>
A; Residues: 1-360 *B
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F86054
BND Polymerage III, beta-subunit [imported] - Escherichia coli (strain O157:H7, substrain C;Species: Escherichia coli
C;Species: Becherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: F86054
R;Perna, N.T.; Plunkett III, G; Burland, V; Mau, B; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Title: Genome sequence
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A;Gene: EC84636
C;Superfamily: DNA-directed DNA polymerase III beta chain
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-366 <STO>
A;Cross-references: GB:AE005174; NID:g12518540; PIDN:AAG58898.1; GSPDB:GN00145; UMGP:251°
A;Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA polymerase III beta-chain [imported] - Salmonella enterica subsp. enterica serovar Ty C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ribarchill, J. Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gacar, P.
Nature 413, 846-852, 2001
A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serove A; A; Complete genome sequence of a multiple drug resistant Salmonella enterica serove A; A; Complete genome sequence of a multiple drug resistant Salmonella enterica serove A; A; Complete genome and Complete genome sequence of a multiple drug resistant Salmonella enterica serove A; A; A; Complete genome and Complete drug complete and Complete genome sequence of a multiple drug resistant Salmonella enterica serove A; A; Residues: preliminary A; A; Residues: Draha, A; Residues: 1-366 cPRR>
A; Cross-references: GB: AL513382; PIDN: CAD03158.1; PID: g16504793; GSPDB: GN00176
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C;Species: Yersinia pestis
C;Date: O2-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
C;Accession: AF0497
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B., R;Parkhill, J.; Wren, B.W.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Invarue 413, 523-527, 2001
Nature 413, 523-527, 2001
A;Fitle: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
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Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
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A.Gene: dnaN
C.Superfamily: DNA-directed DNA polymerase III beta chain
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Query Match 100. Best Local Similarity 100. Matches 5; Conservative

304 EILDV 308

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high affinity transport system protein P37 - Mycoplasma pneumoniae (strain ATCC 29342)
N,Alternate names: hypothetical protein A05_orf380V
C;Species: Mycoplasma pneumoniae
A;VarCC 29342
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Dec-1999
C;Accession: S73751
R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae
A;Reference number: S73327; MUID:97105885; PMID:8948633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA-directed RNA polymerase, subunit A' (rpoA2) homolog - Archaeoglobus fulgidus CiSpecies: Archaeoglobus fulgidus CiSpecies: Archaeoglobus fulgidus C; Species: O5-Dec-1997 #sequence_revision O5-Dec-1997 #text_change 18-Jun-1999 C; Accession: H69485 R. Accession: H69485 R. Accession: H69485 R. A. A. Enou, D. Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997 R. Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N. Smitch, H.O.; Woese, C.R.; Vonter, J.C. A; Artile: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeor, A; Reference number: A69250; MUID:98049343; PMID:9389475
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C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C;Bacesion: B70076
B;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berterc, C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chon A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallerciech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
                                                                                                                                                                                                                                                                                                                                                                                                                        A, Accession: S73751
A, Status: preliminary; nucleic acid sequence not shown; translation not shown
A, Molecule type: DNA
A, Molecule type: DNA
A, Residues: 1-380 < HIM>
A, CCOSS-references: EMBL: AE000041; GB: U00089; NID: 91674104; PIDN: AAB96073.1; PID: 9167411
A, Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
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A;Genetic code: SGC3
A;Start codon: GTG
C;Superfamily: Mycoplasma hyorhinis high affinity transport system protein P37
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100.0%; Score 23; DB 1; Length 380;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
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A;Residues: 1-367 <KMR>
A;Residues: 1-367 <KMR>
A;Residues: 1-367 <KMR>
A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Map position: circular chromosome
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hypothetical protein Atu0249 [imported] - Agrobacterium tumefaciens (strain C58, Dupont) C; Species: Agrobacterium tumefaciens
C; Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C; Accession: A12606
C; Accession: C; Guenthner, D; Kutyavin, T; Levy, R; Li, M; McCleil ; Karp, P; Romero, P; Zhang, S.
Science 294, 2317-2323, 2001
A; Authors: Yoo, H; Tao, Y; Biddle, P; Jung, M; Krespan, W; Perry, M; Gordon-Kamm,
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A;Reference number: AB2577; PMID:11743193
A;Recession: A12606
A;Status: preliminary
A;Molecule type: DNA
A;Residus: 1-367 < KUR>
A;Residus: 1-367 < KUR>
A;Residus: 1-367 < KUR>
A;Cos8-references: GB:AE008688; PIDN:AAL41271.1; PID:g17738578; GSPDB:GN00186
A;Experimental source: strain CS8 (Dupont)
A;Genetics:
A;Genetics:
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                 Length 366;
            100.0%; Score 23; DB 2; Length 36
100.0%; Pred. No. 5.3e+02;
ive 0; Mismatches 0; Indels
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100.0%; Score 23; DB 2; I
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 5; Conservative 0; Mismatches 0;
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306 EILDV 310

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306 EILDV 310

RESULT 67 S73751

1 EILDV S

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137 EILDV 141
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A;Accession: H72323
A;Accession: H72323
A;Accession: H72323
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-386 <ARN>A;Residues: 1-386 <ARN>A;Cross-references: GB:ABC001753; GB:ABC00512; NID:g4981397; PIDN:AAD35959.1; PID:g498141
A;Experimental source: strain MSB8
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portecelle A.; R.; Ogiwar, K.; Schiel, T.M.; Pose, M.; Sadaie, Y.; Sato, T.; Scanlon, A.Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serola akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winthors: Yoshikawa, H.; Danchin, A.; Tosato, V.; Voshida, K.; Authors: Yoshikawa, H.; Danchin, A.; Tosato, V.; Yoshida, K.; Ateference number: A69580; MUID: 98044033; PMID: 9384377
A; Sccession: B70076
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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B70302
C) Depuis Color of the sign protein A - Aquifex aeolicus
C; Species: Aquifex aeolicus
C; Species: Aquifex aeolicus
C; Date: 10-Sep-1999 # Bequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C; Accession: E70302
E; Deckert, G.; Marren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
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C;Superfamily: Helicobacter pylori 2-oxoacid ferredoxin oxidoreductase; 2-oxoacid ferred
C;Keywords: oxidoreductase
F;8-189/Domain: 2-oxoacid ferredoxin oxidoreductase homology <FEO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:299124; GB:AL009126; NID:g2636442; PIDN:CAB15983.1; PID:g2636493
A;Experimental source: strain 168
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A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID;9537320
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A,Gene: yxeP
C,Superfamily: hippurate hydrolase
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Matches 5; Conservative
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Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-380 <KUN>
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A;Accession: E70302
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-402 <AQF>
A;Residues: 1-402 <AQF>
A;Residues: 1-402 <AQF>
A;Cross-references: GB:AE000670; GB:AE000657; NID:g2982779; PIDN:AAC06407.1; PID:g298278;
A;Experimental source: strain VFS
C;Genetics:
A;Gene: mocAl
C;Superfamily: molybdenum cofactor biosynthesis protein mocA-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Arabidopsis thatiana (mouse-car cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 04-Mar-2000
C;Accession: T04821
R;Bevan, M.; Lecharny, A.; Chefdor, F.; Krivitzky, M.; Kreis, M.; Hoheisel, J.; Mewes, Hankerence number: Z15385
A;Reference number: Z15385
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A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic as A;Reference number: A71000, MUID:98344137; PMID:9679194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: strain OT3
A; Note: this accession replaces an interim accession for a sequence replaced by GenBank
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C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0041
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A;Residues: 1-407 <KAW>
A;Cross-references: GB:AP000004; NID:93236131; PIDN:BAA30059.1; PID:93257376
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C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C;Accession: E71087
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A;Introns: 68/1; 110/3; 176/2; 195/2; 221/2; 269/3
A;Note: F10M23.320
C;Superfamily: Arabidopsis thaliana hypothetical protein F10M23.320
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A;Reaidues: 1-403 <BEV>
A;Cross-references: EMBL:AL035440
A;Experimental source: cultivar Columbia; BAC clone F10M23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein F10M23.320 - Arabidopsis thaliana
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Best Local Similarity
Matches 5; Conserv
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Search completed: February 8, 2003, 10:25:02
Job time : 21 secs
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C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: G4-Dec-1986 #sequence_revision 05-Dec-1997 #text_change 01-Mar-2002
C;Accession: H64748; A04451
R;Blattner, F.R; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc
C;Accession: H64748
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Accession: H64748
                                                                                                                                                                                                                                                                                                  Syferal protein - Synechocystis sp. (strain PCC 6803)

hypothetical protein - Synechocystis sp. (strain PCC 6803)

C;Species: Synechocystis sp.

A;Variety: PCC 6603

C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000

C;Accession: S76678

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996

A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
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A,Rebidues: 1-241,S',243-276,'TL',279-396,'KILTKVFRKSPTGS',411,'NA',414,'VKNLLNFANLVKQL
A)Cross-references: GB:M13422, NID:g146255; PIDN:AAA23929.1; PID:g146257
C;Comment: The gene coding for this protein is located between the gpt and phoE genes.
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A; Accession: S76678
A; Status: preliminary
A; Accession: brainary
A; Accession: Grants
A; Residues: 1-408 «KAN»
A; Residues: 1-408 «KAN»
A; Cross-references: EMBL: D64004; GB: AB001339; NID: g1001701; PIDN: BAA10622.1; PID: g120845
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

8, 2003, 10:20:02; Search time 11 Seconds (without alignments) 18.853 Million cell updates/sec February Run on:

US-09-251-073A-16 23

Title: Perfect score:

1 EILDV 5 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 segs, 41476328 residues Searched:

82 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 100% Maximum Match 100% Listing first 100 summaries

SwissProt_40:* **Database**: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

SEQUENCE FROM N.A.
MEDLINE=91088245; PubMed=2124672;
Alonso C., Shirahige K., Ogasawara N.;
"Molecular cloning, genetic characterization and DNA sequence analysis of the reck region of Bacillus subtilis.";
Nucleic Acids Res. 18:6771-6777(1990). Bacillus subtilis. Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus. NCBI_TaxID=1423; (Rel. 21, Created) (Rel. 21, Last sequence update) (Rel. 41, Last annotation update) PRT; 107 AA. YAAK BACSU STANDARD; P242B1; 01-MAR-1992 (Rel. 21, Creat 01-MAR-1992 (Rel. 21, Last 15-JUN-2002 (Rel. 41, Last Hypothetical protein yaaK. YAAK.

121 AA.

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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Aspartate 1-decarboxylase precursor (EC 4.1.1.11) (Aspartate alpha-
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(Rel. 40, Last anno
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                                                                                                                                                                                                                               Wolinella succinogenes.
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Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Borriss R., Boursler L., Brans A., Braun M., Brignell S.C., Bron S.,
Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Bronizof F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
R. Denizof F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
R. Ertia C., Fujita M., Fujita Y., Funa S., Galizzi A., Galleron N.,
R. Hibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
A Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
R. Hibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
A Cobyashi Y., Kochter P., Koningstein G., Krogh S., Kumano M.,
R. Kobayashi Y., Kochter P., Mizuno M., Moeell D., Nakai S., Nuback M.,
A Medina N., Mallado R.P., Liu H., Masuda S., Mauel C., Medigue C.,
R. Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
R. Perescan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
R. Barro V., Pohl T.M., Portetelle D., Porvollik S., Prescott A.M.,
R. Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
Sariguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
Sorokin A., Tacconi E., Takagi T., Tarkemaru K.,
Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vastarotti A.,
Tosato V., Wanbutt R., Wedler H., Wandeler H., Wanters P., Winpat A., Yamamoco Of the Gram-positive bacterium Bacillus
T. The Complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                             Ogasawara N., Nakai S., Yoshikawa H.; Systematic sequencing of the 180 kilobase region of the Bacillus subtilis chromosome containing the replication origin.";
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SEQUENCE 107 Aa, 11781 MW, DB3EBA3420F6A9E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 23; DB 1;
100.0%; Pred. No. 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 390:249-256(1997).
-!- SIMILARITY: BELONGS TO THE UPF0133 FAMILY.
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InterPro; IPR004401; Cons hypoth103.
InterPro; IPR00372; DUF149.
                                                                                                                                                                                                                               MEDLINE=98044033; PubMed=9384377;
                                             MEDLINE=96051385; PubMed=7584024;
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EILDV 56

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                                                                                                                                        Gross R., Simon J., Theis F., Kroeger A.;
"Two membrane anchors of Wolinella succinogenes hydrogenase and their
"Two membrane anchors of Wolinella succinogenes hydrogenase and their
function in fumarate and polysulfide respiration.";
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: L-aspartate = beta-alanine + CO(2).
-!- CATALYTIC ACTIVITY: L-aspartate = beta-alanine + CO(2).
-!- PATHWAY: Pantothenate biosynthesis; second branch.
-!- SIMILARITY: BELONGS TO THE PAND FAMILY.
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CHAIN

SIMILARITY).
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Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
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116-0cT-2001 (Rel. 40, Last sequence update)
16-0cT-2001 (Rel. 40, Last annotation update)
Transcription elongation factor greA (Transcript cleavage factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.
NCBI_TaxID=134821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY). CONVERTED TO A PYRUVOYL GROUP (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 23; DB 1; Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY).
41FB7B63B571F837 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003190; Asp_decarbox.
Pfam; PF02261; Asp_decarbox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=Serovar 3;
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-!- SIMILARITY: BELONGS TO THE CASEIN KINASE 2 BETA CHAIN FAMILY.
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                                                                                                                                                                                                                                                                                       Query Match
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Q58450;
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                                                                                                                                                                                                                               between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                       Transcription regulation; DNA-binding; Coiled coil; Complete proteome.

DOMAIN 7 24 COILED COIL (POTENTIAL).

COILED COIL (POTENTIAL).

SEQUENCE 156 AA; 17767 MW; 86BEA8EC07C96461 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Detailed structure of the Drosophila melanogaster stellate genes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genetics 124:303-316(1990).
--- FUNCTION: RESPONSIBLE FOR THE APPEARANCE OF PROTEINACEOUS STARSHAPED CRYSTALS IN THE PRIMARY SPERMATOCYTES OF D.MELANOGASTER MALES LACKING A Y CHROMOSOME.
--- MISCELLANEOUS: THERE ARE MULTIPLE COPIES OF THE STELLATE GENE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Arthropoda, Mandibulata, Pancrustacea, Hexapoda,
Insecta, Perygota, Neoptera, Endopterygota, Diptera, Brachycera,
Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
NCBI_TaxID=7227,
                                                                       LITE 407.757-762 (2000).

FUNCTION: NECESSARY FOR EFFICIENT RNA POLYMERASE TRANSCRIPTION ELONGATION PAST TEMPLATE-ENCODED ARRESTING SITES. THE ARRESTING SITES IN DNA HAVE THE PROPERTY OF TRAPPING A CERTAIN FRACTION OF ELONGATING RNA POLYMERASES THAT PASS THROUGH, RESULTING IN LOCKED TERNARY COMPLEXES. CLEAVAGE OF THE NASCENT TRANSCRIPT BY CLEAVAGE FACTORS SUCH AS GREA OR GREB ALLOWS THE RESUMPTION OF ELONGATION FROM THE NEW 3'TERMINUS. GREA RELEASES SEQUENCES OF SIMILARITY: BELONGS TO THE GREA/GREB FAMILY.
         Glass J. I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y., Cassell G.H., The complete sequence of the mucosal pathogen Ureaplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 23; DB 1; Length 156; 100.0%; Pred. No. 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                      entities requires a license agreement (Se
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                           HSSP; P21346, 1GRJ; GreA GreB.
InterPro; IPR01437; GreA GreB.
Pfam; PF01272, GreA GreB; 1.
Pfam; PF03449; GreA GreB, 1.
ProDom; PD004918; GreA GreB; 1.
PROSITE; PS00829; GREAB 1; 1.
PROSITE; PS00830; GREAB 2; FALSE NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly)
MEDLINE=20500219; PubMed=11048724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-Oregon-R; TISSUE-Testis;
MEDLINE-90169476; PubMed-1689686;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                               EMBL; AE002128; AAF30713.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                    urealyticum.";
Nature 407:757-762(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transcripts."
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Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stellate protein.
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01-APR-1990
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P15021;
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Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Town J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness B.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Puhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klank H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 23; DB 1; Length 172;
100.0%; Pred. No. 85;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Testis; Multigene famīly.
SEQUENCE 172 AA; 19507 MW; C86304F591E76F8A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Archaea, Buryarchaeota, Methanococci, Methanococcales, Methanocaldococcaceae, Methanocaldococcus.
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Pfam; PF01121; CoaB; 1.
Hypothetical protein; ATP-binding; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: BELONGS TO THE UPF0101 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 36, Created)
(Rel. 36, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                177 AA
                                                                                                                                                                                    entities requires a license agreement (Se
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FROM N.A.
AL-1 / DSM 2661 / ATCC 43067;
                                                                                                                                                                                                                                                                                                                                                                                              FlyBase; FBgn0003523; Ste.
InterPro; IPR000704; CAS Kinase_II.
Pfam; PF01214; CK II beta; 1.
PRINTS; PR00472; CASWKINASEII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS01101; CK2_BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Last an Hypothetical protein MJ1050.
                                                                                                                                                                                                                                                                                              EMBL; X15899; CAA33906.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Methanococcus jannaschii.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                        PIR; S08120; S08120
PIR; S24397; S24397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=2190;
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15-JUL-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T. Structural analysis of Arabidopsis thaliana chromosome 5. VI.

T. Structural analysis of Arabidopsis thaliana chromosome 5. VI.

T. Sequence features of the regions of 1.367,185 bp covered by 19

physically assigned Pl and TAC clones.";

DNA Res. 5:203-216(198).

-!- FUNCTION: RECCONIZES AND BINDS THE THETHYLGUANOSINE-CONTAINING

MENA "CAP" DURING AN EARLY STEP IN THE INITIATION OF PROTEIN

SYNTHESIS AND FACILITATES RIBGOOME BINDING BY INDUCING THE

CONTAINING OF THE MRAAS SECONDRAY STRUCTURES (BY SIMILARITY).

-!- SUBUNIT: EIF4F IS A TRIMER COMPOSED OF EIF4E, BIF4G AND EIF4A

(WHICH CAN CYCLE IN AND OUT OF THE COMPLEX). IN HIGHER PLANTS TWO

ISOPORMS OF EIF4F HAVE BEEN IDENTIFIED, NAMED EIF4F AND

EIF(ISO)4F: EIF4F HAVE BEEN IDENTIFIED, NAMED EIF4F AND

EIF(ISO)4F: EIF4F HAVE GREVENTY PLANTS TWO

-!- SIMILARITY: BELONGS TO THE EUKARYOTIC INITIATION FACTOR 4E FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=cv. Columbia;
MEDLINE=98403884; PubMed=9734815;
Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wittmann S., Chatel H., Fortin M.G., Laliberte J.F.; Interaction of the viral protein genome linked of turnip mosaic potyvirus with the translational eukaryotic initiation factor (1so) 4E of Arabidopsis thaliana using the yeast two-hybrid system.";
                                                                                                                                                                                                                                                                     IFE2_ARATH STANDARD; PRT; 198 AA.

004665; QSGAN8;
15-JUL-1998 (Rel. 36, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Enkaryotic translation initiation factor 4E (eIF-4E) (eIF4E)
subunit) (eIF4Eiso protein) (eIF-(iso)4F 25 kDa subunit) (eIF-(ISO)4F P28
EIF4E2 OR AT5G35620 OR MJE4.8.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                  ö
                                                        Length 177;
                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rodriguez C., Freire M.A., Robaglia C.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
14 ATP (POTENTIAL).
20690 MW; F209572AA79CD2F9 CRC64;
                                                                                                ;
                                                        DB 1;
                                                                            88;
                                                      100.0%; Score 23; DB
100.0%; Pred. No. 88;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=97378268; PubMed=9234949;
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                                                                          Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Virology 234:84-92(1997)
                177 AA;
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NP BIND
SEQUENCE
                                                          Query Match
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HSSP;
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Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
Gurjal M., Hong A., Huizar L., Hyman R.M., Kahn D., Kahn M.L.,
Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
Yeh K.-C., Davis R.W., Federapiel N.A., Long S.R.;
"Nucleotide sequence and predicted functions of the entire
Sinorhizobium meliloti psym Amegaplasmid.";
Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888 (2001).
-!- FUNCTION SCI. U.S.A. 98:9883-9888 (2001).
-!- FUNCTION, SYLARTED OLIGOMER OF N-ACETYLGLUCOSAMINE, THAT
STIMULATES MITOSIS IN VARIOUS PLANT PROTOPLASTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         â
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Egelhoff T.T., Fisher R.F., Jacobs T.W., Mulligan J.T., Long S.R., Nullectide sequence of Rhizobium meliloti 1021 nodulation genes: nodD is read divergently from nodABC."; DNA 4:241-248[1985].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Nodulation protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Toeroek I., Kondorosi E., Stepkowski T., Posfai J., Kondorosi A., "Nucleotide sequence of Rhizobium meliloti nodulation genes.";
Nucleic Acids Res. 12:9509-9524(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmid pSymA (megaplasmid 1).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                    Score 23; DB 1; Length 198;
Pred. No. 99;
                                                                                                                                                                                                                                                                                                                                                              0; Indels
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                                                                                                                                                                                                                         198 AA; 22514 MW; 71FEB309E073A9D2 CRC64;
InterPro; IPR001040; TIF_eIF_4E.
Pfam; PP01652; IP4E; 1.
ProDom; PD003697; TIF_eIF_4E; 1.
PROSITE; PS00813; IF4E; 1.
Initiation factor; Protein biosynthesis; RNA-binding; Multigene family.
SEQUENCE 198 AA; 22514 MW; 71FEB309E073A9D2 CRC64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: TO OTHER POLYSACCHARIDE DEACETYLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P02963; 052477;
21-UL-1986 (Rel. 01, Created)
15-UN-2002 (Rel. 41, Last sequence update)
Chitooligosaccharide deacetylase (EC 3.5.1.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhizobium meliloti (Sinorhizobium meliloti).
                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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MEDLINE=21396509; PubMed=11481432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=1021;
MEDLINE=85229955; PubMed=4006668;
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                                                                                                                                                                                                                                                                                           100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NODB OR RA0474 OR SMA0868.
                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            175 EILDV 179
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MGD; MGI:1928739; Dnajblo.
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229
155
207
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                    229 AA;
                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE PROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6J;
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133
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207
85
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Q9QYIS;
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DISULFID
CARBOHYD
                                                                                                                                                                                                    SEQUENCE
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Matches
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  STTTTTS
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                                                                                                     Smit A.B., Syed N.I., Schaap D., van Minnen J., Klumperman J., Kits K.S., Lodder H., van Der Schors R.C., van Elk R., Sorgedrager B., Brejc K., Sixma T.K., Geraerts W.P.M.;
"A glia-derived acetylcholine-binding protein that modulates synaptic
                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
Acetylcholine-binding protein precursor (ACh-binding protein) (AchBP)
Lymmaea stagnalis (Great pond snail).
Elwaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
Lymmaeidae; Lymmaeidae;
                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MASS SPECTROMETRY: MW-24720.4; METHOD=GTOF; RANGE=20-229.
SIMILARITY: TO THE EXTRACELLULAR PORTION OF LIGAND-GATED IONIC
CHANNELS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 20-229.

MEDLINE=21256199; PubMed=11357122;
Brejc K., van Dijk W.J., Klaaseen V., Schuurmans M.,
van Der Oost J., Smit A.B., Sixma T.K.;
"Crystal structure of an ACh-binding protein reveals the ligand-binding domain of nicotinic receptors.";
Nature 411:269-276(2011).
- FUNCTION: BINDS TO ACETYLCHOLINE. MODULATES NEURONAL SYNAPTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMISSION.
SUBUNIT: HOWOPENTAMER.
SUBCELLULAR LOCATION: SECRETED. RELEASED IN AN ACETYLCHOLINE-
BEPENDENT MANNER IN THE SYNAPTIC CLEFT.
TISSUE SPECIFICITY: EXPRESSED BY GLIAL, CELLS.
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                                                                                                                                                                                                                                                    100.0%; Score 23; DB 1; Length 21
100.0%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                         229 AA
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                                                           EMBL; M11268; AAA98361.1; -.
EMBL; X01649; CAA25809.1; -.
EMBL; AF038577; AAB95330.1; -.
EMBL; AS07237; AAK65132.1; -.
PIR; A03483; ZZZRBM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 411:261-268(2001).
                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTM: N-GLYCOSYLATED.
                                                                                                                                                                                                                                                                             Local Similarity
168 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=6523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transmission."
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P58154;
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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Ohtsuka K., Hata M.;
"Mammalian HSP40/DNAJ homologs: cloning of novel cDNAs and a proposal for their classification and nomenclature.";
Cell Stress Chaperones 5:98-112 (2000).
-: SIMILARITY: CONTAINS 1 J DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95 N-LINKED (GLCNAC. . .) (PROBABLE)
26061 MW; B76A3A13E7EF8FCB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 23; DB 1; Length 229;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACETYLCHOLINE-BINDING PROTEIN
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28601 MW; 81387B09ADF9B09A CRC64;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DnaJ homolog subfamily B member 10 (mDJ8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    259 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                         or send an email to license@isb-sib.ch).
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PROSITE; PS00636; DNAJ_1; FALSE_NEG.
PROSITE; PS50076; DNAJ_2; 1.
                                                                                                                                                                                                                            EMBL, AF364899; AAK64377.1; -.
PDB; 119B; 16-MAY-01.
InterPro; IPR001175; Neur channel.
Pfam; PF02931; Neur chan_LBD; 1.
Pfam; PF02931; Signal; 3D-structure.
SIGNAL
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InterPro, IPR002950; Josephin.
InterPro, IPR003903; UIM.
Pfam; PF00226; DnaJ; I.
Pfam; PF02809; UIM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
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DOMAIN
SEQUENCE
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PRT;

STANDARD;

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Yamamoto Y., Alba H., Baba T., Hayashi K., Inada T., Isono K.,
Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nachimoto H.,
Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasundaram S.,
A Tagami H., Takahashi H., Takeda J., Takemoto K., Uchara K., Wada C.,
A Tamagata S., Horiuchi T.;
T. "Construction of a contiguous 874-kb sequence of the Escherichia coli
T. "Construction of a contiguous 874-kb sequence of the Escherichia coli
T. "Li genome corresponding to 50.0 68 8 min on the linkage map and
analysis of its sequence features.";
DNA Res. 4:91-113(1997).
C. -!- SIMILARITY: BELONGS TO THE HPCH/HPAI ALDOLASE FAMILY.
C. -!- CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
FRAMESHIFT IN POSITION 117.
                                                                                                                                                                                                                                                                                                                                                     MEDINE-97426617; PubMed=9278503; Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                       P76469; P76925; P76928; P76929;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Hypothetical protein yfaU.
YFAU OR B2245.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97349980; PubMed=9205837;
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                     Escherichia coli.
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  YFAU ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stewart V.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROBABLY PART OF A HIGH-AFFINITY BINDING-PROTEIN-
-!- FUNCTION: PROBABLY SYSTEM FOR NITRATE. PROBABLY RESPONSIBLE FOR DEPRENBENT TRANSPORT SYSTEM FOR THE TRANSPORT SYSTEM.
-!- SUBCELLULAR LOCATION: Membrane-associated (Potential).
-!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Klebsiella pneumoniae.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Klebsiella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94222832; PubMed=8169203;
Lin V.T., Goldman B.S., Stewart V.;
"The nasFEDCBA operon for nitrate and nitrite assimilation in
Klebsiella pneumoniae MSal.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 23; DB 1; Length 262; 100.0%; Pred. No. 1.3e+02; tive 0; Mismatches 0; Indels
                             Length 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L27431; AAB86901.1; -.
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003493; ABC_transportr.
Pfam; PP000005; ABC_tran; 1.
ProDom; PD000006; ABC_transportr; 1.
SMART; SM00382; AAA; 1.
TIGRPAMs; TIGRPAMs; TGRO1184; ALCD; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
TRANSPORT; ATP-binding; Membrane; Nitrate assimilation.
NP BIND 4TP (POTENTIAL).
SEQUENCE 262 AA; 28996 MW; AD1B32490A2AEA10 CRC64;
                                                                               0; Indels
                             100.0%; Score 23; DB 1; I 100.0%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                               01-FEB-1995 (Rel. 31, Created)
15-VUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Mitrate transport protein nasD.
                                                                                                                                                                                                                                                                                                                  262 AA
                                                                               0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteriol. 176:2551-2559(1994).
Query Match
Best Local Similarity 100.v.
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                                                                                                                                                                                                                                                                                                                  STANDARD;
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Best Local Similarity
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                                                                                                                               1 EILDV
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                                                                                                                                                                                                                                                             RESULT 10
NASD KLEPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h Score 23; DB 1; Length 267; Similarity 100.0%; Pred. No. 1.4e+02; 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                               EMBL, AE000314; AAC75305.1; -.
EMBL, D90855; BAA16064.1; -.
EMBL, D90855; BAA16064.1; -.
EMBL, D90855; BAA16068.1; ALT_FRAME.
EMBL, D90856; BAA16069.1; ALT_FRAME.
HSSP, P33522; 1DXE.
ECGENE; EG14083; yfaU.
InterPro; IPR05000; HpCH_HpaI.
Frame Pro; IPR05000; HpCH_HpaI.
Frame Pro; IPR05000; HpCH_hpaI.
Frame Profesial processis, 1, yasas; Complete protecome.
SEQUENCE 267 AA; 28916 MW; F68506D8A11D23FE CRC64;
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PURR LACLA
1D PURR LACLA STANDARD; F
C 053065;
DT 15-JUN-2002 (Rel. 41, Created)
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222 EILDV 226

RESULT 11 YFAU_ECOLI

1 EILDV 5

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212 EILDV 216
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P41010;
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Matches
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                                                                                                                                                                                                                                                                                                      SPECIES=L.1.lactis; STRAIN=IL1403;
MEDLINE=21235186; PubMed=11337471;
Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
Weissenbach J., Ehrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacterium Lactococcus
"Tatis sap. lactis IL1403";
Genome Res. 11:731-753(2001).
                                                                                                     Lactococcus lactis (subsp. lactis) (Streptococcus lactis), and Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris). Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus. NCBL_TaxID=1360, 1359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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EMBL; ABC06455; AAK06557.1; -.
InterPro; IPR0008375; FRTransferase.
InterPro; IPR0012375; Frypy rp transf.
Pfam; PF00156; Pribosyltran; 1.
PROSITE; PS00103; PUR_PYR_PR TRANSFER; FALSE NEG.
DNA-binding; Transcription regulation; Repressor; Complete proteome. SEQUENCE 271 AA; 30361 MW; 04614AA24B1C4BCD CRC64;
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Bacillus PS3 (Thermophilic bacterium PS-3).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
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01.MAR-1989 (Rel. 10, Last sequence update)
15.JUN-2002 (Rel. 41, Last annotation update)
ATP synthase gamma chain precursor (EC 3.6.3.14).
15-JUN-2002 (Rel. 41, Last sequence update).
15-JUN-2002 (Rel. 41, Last annotation update).
Pur operon repressor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHOSPHORIBOSYLTRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE PROM N.A.
SPECIES=L.1.cremoris; STRAIN=MG1363;
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Best Local Similarity
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                                                                                           PURR OR LL2259
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ATPG BACP3
AC P09222 BACP3
DT 01-MAR
DT 15-JUM
DE ATP 87/
GN ATPG 87/
CN NEB1 GN
CN NEB1 TR
RY SEQUEN
RY SEQUEN
RA OLEWAY
RA OLEWAY
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RA CLEWAY
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P09222
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-!- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0) HAS THREE MAIN SUBUNITS: A, B AND C.
-!- SIMILARITY: BELONGS TO THE ATPASE GAMMA CHAIN FAMILY.
                                                                                                                                                                                                                                                                                          CORB - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA(1), BETA(1), GAMMA(1), DELTA(1), RPSILON(1). CF(0) HAS THREE MAIN SUBUNITS: A, B AND C. SIMILARITY: BELONGS TO THE ATPASE GAMMA CHAIN FAMILY.
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                                                                                                                                                                                                                                                            -!- SUBUNIT: P-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
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-!- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON GRADIENT ACROSS THE MEMBRANE. THE GAMMA CHAIN IS BELIEVED TO BE IMPORTANT IN REGULATING ATPASE ACTIVITY AND THE FLOW OF PROTONS THROUGH THE CP(0) COMPLEX.
FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON GRADIENT ACROSS THE MEMBRANE. THE GAMMA CHAIN IS BELIEVED TO BE IMPORTANT IN REGULATING ATPASE ACTIVITY AND THE FLOW OF PROTONS THROUGH THE (F(0) COMPLEX.
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                                                                                                                                                                             CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
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TIGREAMS; TIGR01146; ATPBYN F1gamma; 1.
PROSITE; PS00153; ATPASE GAWMA; 1.
Hydrolase; ATP synthesis; CP(1); Hydrogen ion transport.
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01-FEB-1995 (Rel. 31, Last sequence update)
01-FUN-2002 (Rel. 41, Last annotation update)
ATP synthase gamma chain (EC 3.6.3.14).
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Pfam; PF00231; ATP-synt; 1.
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UBIG OR RC0965
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   213 EILDV 217
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                                                                                                   RESULT 16
UBIG_RICCN
ID UBIG_RICCN
AC Q92H07;
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P37269;
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                                                                                                                                                                      SO THE STATE OF STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
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removed. Usage by and for commercial ont (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0) HAS THREE MAIN SUBUNITS: A, B AND C. SIMILARITY: BELONGS TO THE ATPASE GAMMA CHAIN PAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

Ishizuka M., Imai H.;

Submitted (AUG-1994) to the EMBL/GenBank/DDBU databases.

-1- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
GRADIENT ACROSS THE MEMBRANE. THE GAMMA CHAIN IS BELIEVED TO BE
IMPORTANT IN REGULATING ATPASE ACTIVITY AND THE FLOW OF PROTONS
THROUGH THE CF(0) COMPLEX.

-1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 287;
                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 23; DB 1; Length 28
100.0%; Pred. No. 1.5e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                               InterPro; IPR000131; ATPase_gamma.
Pfam; PF00031; ATP-Bynt; 1.
PRINTS; PR00126; ATPASEGAMMA.
TIGRFAMM; TIGR01146; ATPSYM FIgamma; 1.
PROSTIE; P800155; ATPASE GAMMA; FALSE NEG.
ATP SYNTHesis; CF(1); Hydrogen ion transport; Hydrolase.
SEQUENCE 287 AA; 32343 MW; BA039503BDIFIE5A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro; IPR000131; ATPase_gamma.
Pfam; PF00231; ATP-synt; 1.
PRINTS; PR00126; ATPASCAWAA.
TIGRPAMS; TIGR01146; ATPSYN FIgamma; 1.
PROSITE; PS00155; ATPASE GAWMA; FALSE NEG.
ATP Synthesis; CF(1); Hydrogen ion transport; Hydrolase.
SEQUENCE 287 AA; 32391 MW; 78A9FB92E01BAE6E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Firmicutes; Bacillales; Geobacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ATP synthase gamma chain (EC 3.6.3.14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              287 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                   entities requires a license agreement (
or send an email to license@isb-sib.ch)
       not
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and this statement is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus stearothermophilus
                                                                                                                                   EMBL; D38058; BAA07247.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    213 EILDV 217
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P42007;
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ATPG BACST

DATPG BACST

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
Science 293:2093-2098 (2001).
-!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3-
demethylubiquinone-9 = S-adenosyl-L-homocysteine + ubiquinone-9.
-!- PATHWAY: Ubiquinone biosynthesis
-!- SIMILARITY: BELONGS TO THE UBIG/COQ3 FAMILY.
-!- SIMILARITY: CONTAINS I RPEI INSERT DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=Malish 7;
MEDLINE=21442074; PubMed=11557893;
Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
Raoult D.;
                                                       15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
3-demethylubiquinone-9 3-methyltransferase (EC 2.1.1.64) (3,4-dihydrxyy-5-hexaprenylbenzoate methyltransferase) (DHHB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBL_TaxID=781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Symechococcus sp. (strain PCC 7942) (Anacystis nidulans R2)
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 23; DB 1; Length 289;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE008649; AAL03503.1; -.
InterPro; IPR001601; Methyltransf.
InterPro; IPR000051; SAM bind.
IIGRFAMS; ITGR01045; RPB; 1.
Ubiquinone biosynthesis; Transferase; Methyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RPE1 INSERT.
4CAEA6827EC78977 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-UTN-2002 (Rel. 41, Last annotation update)
Phytoene synthase (EC 2.5.1.-).
   289 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  307 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (Se
or send an email to license@isb-sib.ch).
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STANDARD;
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                                                                                                                                                                                                        metĥyltrânsferase).
                                                                                                                                                                                                                                                                   Rickettsia conorii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         289 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome.
DOMAIN 50
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protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phosphatase-1
                                                                                                                                                                                                                                                 38 EILDV 42
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P22194;
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                                                                                                                                                                         Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=ATCC 29342 / M129;
MEDLINE=Z108919; PubMed=11271496;
REGULA J.T., Ueberle B., Boguth G., Goerg A., Schnoelzer M.,
Herrmann R., Frank R.;
"Towards a two-dimensional proteome map of Mycoplasma pneumoniae.";
Blectrophoresis 21:3765-3780(2000).
-i- SIMILARITY: BELONGS TO THE NUSG FAMILY.
                                                                                              CATALYTIC ACTIVITY: 2 geranylgeranyl diphosphate = diphosphate prephytoene diphosphate.
                                                                                                                                             PATHWAY: Carotenoid biosynthesis.
SIMILARITY: BELONGS TO THE PHYTOENE/SQUALENE SYNTHETASE FAMILY
         Chamovitz D., Misawa D., Sandmann N., Hirshberg J.;
Molecular cloning and expression in Escherichia coli of a
cyanobacterial gene coding for phytoene synthase, a carotenoid
biosynthesis enzyme.;
FEBS Lett. 296:305-310(1992).
TO PHYTOENE TO PHYTOENE DIPHOSPHATE
TO PHYTOENE.
                                                                                                                        CATALYTIC ACTIVITY: Prephytoene diphosphate = diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycoplasma pneumoniae.
Bacteria, Firmicutes, Mollicutes, Mycoplasmataceae, Mycoplasma.
                                                                                                                                                                                                                                                                                                                                PROSITE; PS01044; SQS PSY; 1. PROSITE; PS01044; SQUALEN PHYTOEN SYN 1; 1. PROSITE; PS01045; SQUALEN PHYTOEN SYN 2; 1. Multifunctional enzyme; Carotenoid biosynthesis; Transferase. SEQUENCE 307 AA; 35781 MW; A138425F66D10EB8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 23; DB 1; Length 307; 100.0%; Pred. No. 1.6e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDENTIFICATION BY MASS SPECTROMETRY, AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                              PIR; S22200; S22200.
PIR; S20383; S20383.
InterPro; IPR002060; Squ/phyt_synthse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic Acids Res. 24:4420-4449(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein MG054 homolog (D09_orf320)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=ATCC 29342 / M129;
MEDLINE=97105885; PubMed=8948633;
 MEDLINE=92164786; PubMed=1537409;
                                                                                                                                                                                                                                                                                     EMBL; X63873; CAA45350.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=2104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     269 EILDV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Herrmann R.;
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Mod V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Squores J., Peat N., Hayles J., Baker S., Basham D., Bowaman S., Brown D., Brown B., Ellingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Horneby T., Howarth S., Huchel E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Money P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., O'Nell S., Parasarson D., Quail M., Rabbinowitsch B., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Skelton J., Volckaert G., Aert R., Robben J., Grymonprez B., Weltjens I., Vanstreels B., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Berzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Purnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottler S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Obkura H., Yanagida M.;
Obkura H., Yanagida M.;
"S. pombe gene sds22+ essential for a midmitotic transition encodes a
leucine-rich repeat protein that positively modulates protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stone E.M., Yamano H., Kinoshita N., Yanagida M., Mitotic regulation of protein phosphatases by the fission yeast
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 320;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  320 AA; 36107 MW; ECE3C626C8EAE63F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1991 (Rel. 19, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Protein phosphatases PP1 regulatory subunit sds22.
SDS22 OR SPAC4A8.12C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 23; DB 1; L 100.0%; Pred. No. 1.7e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              332 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND CHARACTERIZATION.
                                                                                                                                                                                                                                                             EMBL; AE000011; AAB95735.1; ...
InterPro; IRR001662; NueG.
Pfam; PF02357; NueG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91098642; PubMed=1846086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ilarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sell 64:149-157(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
les 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome. SEQUENCE 320 AA;
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NCBI_TaxID=60217;
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                                                                                                                                                    FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shewanella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 BILDV
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ID DHAS SHEVI
AC Q56734;
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                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.; The genome sequence of Schizosaccharomyces pombe."; Nature 415:871-88 (2002).

-I - FUNCTION: ESSENTIAL FOR THE MITOTIC METAPHASE/ANAPHASE TRANSITION POSITIVELY MODULATES PROTEIN PHOSPHATASE-1. POSSIBLY BY FORMING A PEPRATING HELICAL ROD THAT IS CAPABLE OF ENHANCING A PP1-DEPENDENT DEPHOSPHORYLATIVE AND ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-0C7-2001 (Rel. 40, Last annotation update)
Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11) (ASA dehydrogenase)
(ASADH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shewanella sp. (strain DB6705).
Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
                                                                                                                                                                                     SIMILARITY: CONTAINS 8 LEUCINE-RICH REPEATS (LRR). SIMILARITY: STRONG, TO YEAST SDS22 AND C.ELEGANS T09A5.9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 23; DB 1; Length 332; 100.0%; Pred. No. 1.7e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00560; LRR; 8.
SMART; SM00370; LRR; 10.
SMART; SM00446; LRRcap; 1.
Leucine-rich repeat; Repeat; Mitosis; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CF7FBAD984E2A345 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              338 AA
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LERR 2.
LERR 4.
LERR 5.
LERR 6.
LERR 6.
LERR 7.
LERR 8.
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EMBL; Z98762; CAB11482.1; -.
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                                                                                                                                                              SUBCELLULAR LOCATION: Nuclear. PTM: PHOSPHORYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38066 MW;
                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001611; LRR.
InterPro; IPR003592; LRR out.
InterPro; IPR003603; LRRCap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Conservative
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                                                                                                                                                                                                                                                                                                                                     PIR; A38439; A38439.
HSSP; P09661; 1A9N.
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332 AA;
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Best Local Similarity
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                                                                                                                                                    PHOSPHATASES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 EILDV 244
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Q56732;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
Kato C., Smorawinska M., Li L., Horikoshi K.;
"Comparison of the gene expression of aspartate beta-D-semialdehyde dehydrogenase at elevated hydrostatic pressure in deep-sea bacteria.";
J. Blochem. 121:717-723 (1997).
-!- CATALYTIC ACTIVITY: L-aspartate-4-semialdehyde + phosphate +
NADP(+) = L-4-aspartyl phosphate + NADPH.
-!- PATHWAY: SECOND STEP IN THE COMMON BIOSYNTHETIC PATHWAY LEADING
FROM ASP TO THE CELL WALL PRECURSOR MESO-DIAMINOPIMELATE, TO LYS,
TO MET, TO ILE AND TO THR.
-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11) (ASA dehydrogenase)
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Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 23; DB 1; Length 338;
Pred. No. 1.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000319, Asp semiald dh.
InterPro; IPR000319; Semialdh dh.
InterPro; IPR000534; Semialdh dh.
InterPro; IPR000534; Semialdhyde dh; 1.
Pfam; PF02174; Semialdhyde dh; 1.
ITGRFAMS; ITGRR01296; asd B; 1.
PROSITE; PS01103; ASD; FĀLSE NEG.
Oxidoreductase; NADP; Diaminopimelate biosynthesis;
Inysine biosynthesis.
ACT SITE 132 132 BY SIMILARITY.
SEQÜENCE 338 AA; 36984 MW; 6BCD8921E4977185 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
GECD8921E4977185 CRC64;
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MEDLINE=97306055; PubMed=9163523;
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Query Match
Best Local Similarity 100...
Best Si Conservative
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modified and this statement is not removed.
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342 AA;
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Best Local Similarity
Matches 5; Conserv
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P52610;
                                                                                                                                                                                                                                                                       SEQUENCE
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REPEAT
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                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swies Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of Clostridium perfringens.",
Mol. Gen. Genet. 243:215-224(1994).
-!- CATALYIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages between N-
acetyl-D-glucosamine and N-acetylmuramic acid in peptidoglycan
heteropolymers of the prokaryotes cell'walls.
-!- SIMILARITY: BELONGS TO FAMILY 25 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Canard B., Garnier T., Saint-Joanis B., Cole S.T.; "Molecular genetic analysis of the nagH gene encoding a hyaluronidase
                                                                                                                                                                                                                                                                                                                                       Gaps
SIMILARITY: BELONGS TO THE ASPARTATE-SEMIALDEHYDE DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A., Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H., "Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clostridium perfringens.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                           100.0%; Score 23; DB 1; Length 338; 100.0%; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                  338 AA; 37061 MW; 8D0DC1F46EAF30AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1992 (Rel. 23, Created)
15-UUN-2002 (Rel. 41, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
Probable autolytic 1ysozyme (EC 3.2.1.17) (1,4-beta-Nacetylmuramidase) (Autolysin).
                                                                                                                                                                                                                TIGRFAMB; TIGR01296; asd B; 1.
PROSITE; PS01103; ASD; FĀLSE_NEG.
Oxidoreductase; NADP; Diaminopimelate biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:996-1001 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       342 AA.
                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                       BY SIMILARITY
                                                                                                                                                                 InterPro, IPR000319; Asp_semiald_dh.
InterPro, IPR0000534; Semialdh_dh.
Pfam; PF01118; Semialdhyde_dh; I.
Pfam; PF02774; Semialdhyde_dhc; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                       EMBL; D49540; BAA08490.1; -. HSSP; P00353; 1BRM.
                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                    132
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STRAIN=13 / Type A;
PubMed=11792842;
                                                                                                                                                                                                                                                         Lysine biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1502;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      LYC CLOPE
P26836;
                                                                                                                                                                                                                                                                                   SEQUENCE
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oved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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MEDLINE=9806594; PubMed=9403685;
Praser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
van Yugt R., Palner N., Adams M.D., Gocayne J.D., Weidman J.,
Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
Garland S., Pujil C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dunn J.J., Butler-Loffredo L., Kieleczawa J., Medalle J., Luft B.J.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 23; DB 1; Length 342; 100.0%; Pred. No. 1.8e+02; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EC3B4078A2FB4732 CRC64;
                                                                                             EMBL; AP003186; BAB80088.1; -.
EMBL; M81878; AAA23261.1; -.
InterPro; IPR002053; GH 25.
InterPro; IPR003646; SH3 bac.
Pfam; PF01183; Glyco_hydro_25; 1.
SMART; SM00287; SH3, 2.
PROSTIE; P800953; GLYCOSYL HYDROL F25; 1.
Hydrolase; Glycosidase; Bacteriolytic enzyme; Repeat;
                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
BY SIMILARITY.
5 X 23 AA TANDEM REPEATS.
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SUBCELLULAR LOCATION: INNER MEMBRANE-ASSOCIATED
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Borrelia burgdorferi (Lyme disease spirochete)
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
NCBL_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last Bequence update)
10-CCT-2001 (Rel. 40, Last annotation update)
Flagellar motor switch protein flig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           344 AA.
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-!- SIMILARITY: BELONGS TO THE FLIG FAMILY.
                      entities requires a license agreement (Se or send an email to license@isb-sib.ch).
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15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DnaJ homolog subfanily B member 2 (Heat shock 40 kDa protein homolog 1) (HSJ-1).
DNAJB2 OR HSJ1 OR HSPF3.
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Cheerham M.B.;
Submitted (JUL-1998) to the SWISS-PROT data bank.
-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; HSJ1A AND HSJ1B (SHOWN HERE);
ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: BRAIN (NEURONAL LAYERS). WEAKLY, IN SKELETAL
MUSCLE AND SPLEEN.
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Mammalla, Butheria, Primates, Catarrhini, Hominidae, Homo.
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"Human homologues of the bacterial heat-shock protein DnaJ are
preferentially expressed in neurons.";
Blochem. J. 284:465-476(1992).
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EMBL; X63368; CAA44969.1; ALT_SEQ.
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MEDLINE=92287055; PubMed=1599432;
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HSSP; Q9WY63; 1QC7.
TIGR; BB0290;
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Best Local Similarity
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MEDLINE-84237568; PubMed=6234204;
Obmort H., Kimura M., Nagata T., Sakakibara Y.;
"Structural analysis of the dnaA and dnaN genes of Escherichia coli.";
Gene 28:159-170(1984).
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MEDLINE=93315143; PubMed=7686882;
Burland V.D., Plunkett G. III, Daniels D.L., Blattner F.R.;
"DNA sequence and analysis of 136 kilobases of the Escherichia coligenome: organizational symmetry around the origin of replication.";
Genomics 16:551-561(1993).
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MEDLINE=21074935; PubMed=11206551;

MEDLINE=21074935; PubMed=11206551;

Rena N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfal G., Hackett J., Kilnk S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.;

"Genome sequence of enterchaemorrhagic Escherichia coli O157:H7.";

Nature 409:529-533(2001).
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Escherichia coli 0157:H7.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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351 MISSING (IN ISOFORM HSJIA).
38783 MW; 1FA290C6764665F3 CRC64;
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01-APR-1988 (Rel. 07, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
DMA Polymerase III, beta chain (EC 2.7.7.7).
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InterPro; IPR003903; UIM.
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Pfam; PF03809; UIM; 2.
SMART; SMO0271; DnaJ; 1.
PROSITE; PS00636; DNaJ_1; 1.
PROSITE; PS50076; DNAJ_2; 1.
                                                                                         InterPro; IPR001623; DnaJ.N.
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Genew; HGNC:5228; DNAJB2
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                                            MIM; 604139;
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            AE000447; AAC76724.1;
AE005601; AAG58898.1;
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Biocessays 14:105-111(1992)

The Every Processor of The Replicative Synthesis in Bacteria.

The Bernorlon: DNA POLYMERASE III IS A COMPLEX, MULTICHAIN ENZYME

THIS DNA POLYMERASE ALSO EXHIBITS 3' TO 5' EXONUCLEASE ACTIVITY.

THE BETT CHAIN IS REQUIRED FOR INITIATION OF REPLICATION ONCE IT

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MEDLINE-84297235; PubMed-6089112;
Adachi T., Mizuuchi K., Menzel R., Gellert M.;
"DNA sequence and transcription of the region upstream of the E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Accessory protein function in the DNA polymerase III holoenzyme from \mathbf{E}. coli.";
                                                                                                                                                                                                                                            SEQUENCE OF 143-170 FROM N.A.
MEDLINE=86301872; PubMed=3527871;
Armengod M.B.E., Lambies E.;
"Overlapping arrangement of the recF and dnaN operons of Escherichia coli; positive and negative control sequences.";
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 297-366 FROM N.A.
MEDLINE-84272665; PubMed-6379647;
Blanar M.A., Sandler S.J., Armengod M.-E., Ream L.W., Clark A.J.;
"Molecular analysis of the recF gene of Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 81:4622-4626(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
MEDLINE-92257585; PubMed=1349852;
Kong X.-P., Onrust R., O'Donnell M., Kuriyan J.;
Kong X-dimensional structure of the beta subunit of E. coli DNA
polymerase II holocenzyme: a sliding DNA clamp.";
Cell 69:425-437(1992).
Kuhara S., Shiba T., Hattori M., Shinagawa H.; Complete genome sequence of enterchemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12."; DNA Res. 8:11-22(2001).
                                                                                                                              MEDLINE-88298898; PubMed-2841344;
Armengod M.E.E., Garcca-Sogo M., Lambies E.;
Transcriptional organization of the dnaN and recF genes of Escherichia coli K-12.";
J. Biol. Chem. 263:12109-12114(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 12:6389-6395(1984).
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EMBL; L10328; AAA62052.1; -.
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SEQUENCE OF 1-14 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     + {DNA}(N).

**EUNIT: CONTAINS A CORE (COMPOSED OF ALPHA, EPSILON, AND THETA CHAINS) THAT ASSOCIATES WITH A TAM SUBUNIT WHICH ALLOW THE CORE DIMERIZATION TO FORM THE POLILI' COMPLEX. POLILI' ASSOCIATES WITH THE GAMMA, OBLITA, DELTA, DELTA, PSI, COMPLEX IS: (CAMPOSED OF CHAINS GAMMA, DELTA, DELTA', PSI, COMPLEX IS: (ALPHA, EPSILON, THE TAM [2] - (GAMMA, DELTA, DELTA', BSI, CHI) [2] - BETA [4].

**SUBCELLULAR LOCATION: CYtoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Kan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K., "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Skovgaard O., Hansen F.G.;

"Comparison of dnaA nucleotide sequences of Escherichia coli,
"Comparison of dnaA nucleotide sequences of Escherichia coli,
salmonalla typhimurium, and Serratia marceacens.";
J. Bacteriol. 169:3976-3981(1987).

-i- FUNCTION: DNA POLYMERASE III IS A COMPLEX, MULTICHAIN ENZYME
RESPONSIBLE FOR MOST OF THE REPLICATIVE SYNTHESIS IN BACTERIA.
THIS DNA POLYMERASE ALSO EXHIBITS 3' TO 5' EXCONDULBASE ACTIVITY.
THE BETA CHAIN IS REQUIRED FOR INITIATION OF REPLICATION ONCE IT
IS CLANDED ONTO DNA, IT SLIDES FREELY (BIDIRECTIONAL AND ATP-
INDEPRNDENT) ALONG DUPLEX DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella typhimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                     ö
                                                                    Length 366;
                               100.0%; Score 23; DB 1; Length soil no.0%; Pred. No. 1.9e+02; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amini F., Blinkova A., Walker J.R., Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases
364
40586 MW; 7A45646F61255B5A CRC64;
                                                                                                                                                                                                                                                                                                                         DP3B SALTY STANDARD; PRT; 366 AA. P26464; O50240; 01-AUG-1992 (Rel. 23, Created) 15-DE-1998 (Rel. 37, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) DNA polymerase III, beta chain (EC 2.7.7.7).
                                                                                        Local Similarity 100.0%; Pred. No. 1.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-LIZ / SGSC1412 / ATCC 700720;
MEDLINE-21534948; PubMed=11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=87307970; PubMed=3040670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-62 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 413:852-856(2001).
364 3
366 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNAN OR STM3837.
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                                                                                                                                                                                                           304 EILDV 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=LT2;
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STRAND
SEQUENCE
                                                                    Query Match
                                                                                                                                                                                                                                                                             RESULT 26
DB3B SALIY
DB3B SALIY
DB464
DT 101-AUG
DB DNA POI
OS SALMONIO
OS SAL
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-!- FUNCTION: P37 IS PART OF A HIGH-AFFINITY TRANSPORT SYSTEM.
-!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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ENBL, ARO00041; AAB96073.1; -...

PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.

Transport; Membrane; Lipoprotein; Signal; Complete proteome.

Transport; Membrane; Lipoprotein; High AFFINITY. TRANSPORT SYSTEM PROTEIN

HIGH AFFINITY TRANSPORT SYSTEM PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycoplasma pneumoniae.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2104;
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EMBL; AF034747; AAB87631.1; -
EMBL; AE008879; AAL22696.1; -
EMBL; MA7352; AAA02816.1; -
HSSP; PO0583; AAA02816.1; -
StyGene; SG10089; dnaN.
StyGene; SG10089; dnaN.
StyGene; SG10089; dnaN.
StyGene; PF00710; DNA_DO13_Deta, 1.
Pfam; PF02767; DNA_DO13_Deta_2; 1.
Pfam; PF02768; DNA_DO13_Deta_2; 1.
SNART; SM0480; POL3136; 1.
TIGRFAMS; TIGRF00663; dnan; 1.
TIGRFAMS; TIGRF00663; dnan; 1.
TTANSFERSE; DNA-directed DNA polymerase; DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 23; DB 1; Length 366; 100.0%; Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         41 T -> A (IN REF. 3).
366 AA, 40548 MW, 575FD8F13D928742 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P37 MYCPN STANDARD; PRT; 380 AA.
P75371;
01-NOV-1997 (Rel. 35, Created)
11-NOV-1997 (Rel. 35, Last sequence update)
116-OCT-2001 (Rel. 40, Last annocation update)
1910 affinity transport system protein P37 precursor.
P37 OR MP9415 OR MP425.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
MEDLINE-97105885; PubMed-8948633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome.
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Bacillus subtilis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
Hypothetical protein yxeP.
YXEP OR LPGH
                                                           NCBI_TaxID=1423;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                           SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

XIENTH-WC-16, DSM 4304 / ATCC 49558;

XIENTH-WC-16, DSM 4304 / ATCC 49558;

XIENTH-B-98049343; PubMed=939475;

XIENTH-P., Clayton R.J., Tomb J.-F., White O., Nelson K.E.,

XIENTH-B-N. Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,

XIENTH-BRANCH R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,

XIENTH-BRANCH R.D., MCKENH-SH., MCKENH-SH., Sutton G.G., Gill S.,

XIENTH-BRANCH R.D., Weiden J.F., McDonald L., Utterback T.,

XOVET-BER, GGCSANH J.D., Weiden J.F., McDonald L., Utterback T.,

X Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,

A Wenter J.C.;

X Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 23; DB 1; Length 380; 100.0%; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002879; RNA pol A2.
Pfam; PP01854; RNA pol A2; 1.
Transferase; Transcription; DNA-directed RNA polymerase;
Complete proteome.
SEQUENCE 380 AA; 42422 MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                            Archaea; Buryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
18-OCT-2010 (Rel. 40, Last annotation update)
RNA-directed RNA polymerase subunit A" (EC 2.7.7.6).
RPOA2 OR AP1889.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 41, Last annotation update)
                                                                         380 AA
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                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                Archaeoglobus fulgidus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 5; Conserv
                                                                                                                                                                                                       NCBI_TaxID=2234;
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98 EILDV 102
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         370 EILDV 374
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01-OCT-1996
15-JUN-2002
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YXEP_BACSU
ID _YXEP_BACSU
AC P54955;
                                                          RPA2_ARCFU
ID RPA2_ARCFU
AC 028390;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RAK Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Brington J.J., Connerton I.P., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.P., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmercon P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Chones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Rieger M., Rivolta C., Rocha B., Ropoport G., Rey M., Sadaie Y.,
Sachleich S., Schroceter R., Scoffone F.,
Sckiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
Sekiguchi J., Sekowska A., Seror S.J., Serror P., Yasamotot A.,
Narda A., Wambutt R., Wedler E., Walder E., Wahner K., Vasumoto K., Yata K.,
Whiters P., Wabbata H.F., Zumschein E., Yoshikawa H., Danchin A.,
The Complete genome sequence of the Gram-positive bacterium Bacillus
T. The The The Transfer C., Th
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                                    STRAIN=168 / BGSCIA1;
MEDLINE=97021444; PubMed=8867804;
Yoshida K.-I., Fujimyra M., Yanai N., Fujita Y.;
Toloning and sequencing of a 23-kb region of the Bacillus subtilis genome between the iol and hut operons.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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InterPro; IPR002933; Peptidase M20.

InterPro; IPR002933; Peptidase M20.

Pfam; PF01546; Peptidase M20; I.

Hypothetical protein; Hydrolase; Complete proteome.

SEQUENCE 380 AA; 41596 MW; BD149964FAE42118 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 390:249-256(1997).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D45912; BAA08332.1; -. EMBL; Z99124; CAB15983.1; -.
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les 5; Conserv
                                                                                                                                                                                                                                                                                                                                               [2]
SEQUENCE PROM N.A.
SEQUENCE FROM N.A.
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277 EILDV 281

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44 EILDV

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UDDUDISHED OBSERVATIONS (JAN-2000).

-I- FUNCTION: THE B REGULATORY SUBUNIT MIGHT MODULATE SUBSTRATE SELECTIVITY AND FACTALITY, AND ALSO MIGHT DIRECT THE SELECTIVITY AND FACH SOME TO A PARTICULAR SUBCELLULAR COMPARTMENT. INTERACTS WITH CYCLIN G (IN VITRO).

-I- SUBUNIT: PP2A CONSISTS OF A COMMON HETERODIMERIC CORE ENZYME, COMPOSED OF A SE AD ACCOMONITY (SUBUNIT C) AND A 65 KDA CONSTANT REGULATORY SUBUNIT (RAS OF A SECULATORY SUBUNIT).

WITH A VARIETY OF REGULATORY SUBUNITS. PROTEINS THAT ASSOCIATE WITH THE CORE DIMER INCLUDE THREE FAMILLES OF REGULATORY SUBUNITS B (THE R2) FAPES SHESS), THE 48 KDB VARIABLE REGULATORY SUBUNITS, VIRAL PROTEINS, AND CELL SIGNALING MOLECULES.
                                                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last sanctation update)
Serine/threonine protein phosphatase 2A, 56 kDa regulatory subunit, epsilon isoform (PSZA, B subunit, B epsilon isoform) (PPZA, B subunit, B subunit, B56 epsilon isoform) (PPZA, B subunit, RF subunit, R5 epsilon isoform) (PPZA, B subunit, R61 epsilon isoform) (PPZA, B subunit, R7 epsilon isoform)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: BELONGS TO THE PHOSPHATASE 2A REGULATORY SUBUNIT B
                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'p53-dependent association between cyclin G and the B' subunit of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Embryonic fibroblast;
MEDLINE-97042488; PubMed-8887688;
Okamoto K., Kamibayashi C., Serrano M., Prives C., Mumby M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45497 MW; 780D5404848A548E CRC64;
   387 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDENTIFICATION OF PROBABLE FRAMESHIFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, U49728; AAB37234.1; ALT_FRAME.
MGD; MGI:1349473; Ppp2r5e.
InterPro; IPR002554; B56.
Pfam; PF01603; B56; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein phosphatase 2A.";
Mol. Cell. Biol. 16:6593-6602(1996).
   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Conservative
       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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2ASE MOUSE
Q61151;
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                                             SOLUTION SOL
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                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 93:4638-4643(1996).
-!- FUNCTION: MAY SERVE AS "FLLIPPASE" AS WELL AS A GLUCOSYLTRANSFERASE
-!- THAT TRANSFERS GLUCOSE TO CERAMIDE.
-!- CATALYTIC ACTIVITY: UDP-glucose + N-acylsphingosine = UDP + D-
                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ceramide glucosyltransferase (EC 24.1.80) (Glucosylceramide synthase)
(GCS) (UDP-glucose:N-acylsphingosine D-glucosyltransferase) (GLCT-1).
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=95209704; PubMed=8643456;
IChikawa S., Sakiyama H., Suzuki G., Hidari K.I.-P., Hirabayashi Y.;
"Expression clonning of a cDNA for human ceramide glucosyltransferase that catalyzes the first glycosylation step of glycosphingolipid
                                                                                                                                                                                                                                                                                                                                                                                                                                 glucosyl-N-acylsphingosine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001173; Glycos transf_2.
Pfam; PF00535; Glycos transf_2; 1.
Transferase; Glycosyltransferase; Transmembrane; Signal-anchor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- TISSUE SPECIFICITY: FOUND IN ALL TISSUES EXAMINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LUMENAL (POTENTIAL).
SIGNAL-ANCHOR (POTENTIAL)
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; Pred. No. 2.1e+02;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YAFA ECOLI STANDARD; PRT; 414 AA. P04335; P77413; 20-MAT-1987 (Rel. 04, Created) L5-UN-2002 (Rel. 41, Last sequence update) 15-UN-2002 (Rel. 41, Last annotation update) Hypothetical protein yafA.
                                  394 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                  STANDARD;
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DOMAIN
                                                                                                                                                                      Homo sapiens (Human)
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394 AA;
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                                                                                                                                                                                                                        NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                              synthesis.";
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                                  CEGT HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EILDV
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                                                016739;
RESULT 31
CEGT_HUMAN
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YAFA ECOLI
ID YAFA E
AC P04335
DT 20-MAR
DT 15-JUN
DE HYPOCH
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                                                                                                                                                                                                                                                                                    MEDLINE=21534948; PubMed=11677609; McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Materston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2ASG MOUSE STANDARD; PRT; 415 AA.

060956; 035708;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Serinefhrenonine protein phosphatease 2A, 56 kba regulatory subunit, gamma isoform (PP2A, B subunit, B' gamma isoform) (PP2A, B subunit, B' gamma isoform) (PP2A, B subunit, RS gamma isoform) (PP2A, B subunit, RS gamma isoform) (PP2A, B subunit, B' sahent).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bryant D.W., Rossetto F.E., O'Reilly C., Nieboer E., Turnbull J., Submitted (NOV-1991) to the EMBL/GenBank/DDBJ databases
                                                                                                                                Salmonella typhimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95004589; PubMed=7920643;
Robison K., Gilbert W., Church G.M.;
"Large scale bacterial gene discovery by similarity search.";
Nat. Genet. 7:205-214(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 23; DB 1; I
100.0%; Pred. No. 2.2e+02;
                    01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein yafA.
YAFA OR STM0318.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=LT2 / SGSC1412 / ATCC 700720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE008709; AAL19274.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-36 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 413:852-856(2001).
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nes 5; Conserv
                                                                                                                                                                                                 NCBI_TaxID=602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDENTIFICATION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=LT2;
                                                                                                                                                                            Salmonella.
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1D 2ASG W

AC 060976.1

DT 30-MAY-

DT 30-MAY-

DT 30-MAY-

DE Gamma 10-

DE Gamma 10-

DE BSG gamma 10-

DE BSG Gamma 10-

DE BSG Gamma 10-

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  8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAID=KI2 / W3110;
STRAID=KI2 / W3110;
Takemoto K., Mozi H., Murayama N., Kataoka K., Yano M., Itoh T.,
Yamamoto Y., Inokuchi H., Miki T., Hatada E., Fukuda R., Ichihara S.,
Mizuno T., Makino K., Nakata A., Yura T., Sampei G., Mizobuchi K.;
Systematic sequencing of the Escherichia coli genome: analysis of the
4.0 - 6.0 min (189,987 - 281,416bp) region.";
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NV -> TL (IN REF. 1 AND 3).
NPDKGLAGITUPWIEKKEL -> KILTKVFRKSPTGSKNACV
KNLINFANLVKQLHHNRR (IN REF. 1 AND 3).
2CLSF846CPC9565E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                        STRAIN=K12 / MGI655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Schramm S., Duncan M., Allen E., Araujo R., Aparicio A., Chung E.,
Davis K., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O.,
Lashkari D., Lew H., Lin D., Namath A., Oefner P., Roberts D.,
                                                                                                                                                MEDLINE=85155481; PubMed=6397401; Musech J., Schumperli D.; Nuesch J., Schumperli D.; Structural and functional organization of the gpt gene region of Escherichia coll."; Gene 32:243-249(1984).
                           Bacteria, Proteobacteria, gamma subdivision, Enterobacteriaceae,
Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                           "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Davis R.W.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 1 AND 3).
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EcoGene; EG11091; yafA.
InterPro; IPR000379; Ser_estrg_site.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      414 AA; 47008 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M13422; AAA23929.1; -. EMBL; AE000132; AAC73343.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D83536; BAA77908.1; -.
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Best Local Similarity 100...
S; Conservative
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414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein;
                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                       Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          397
                                                                                  NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69
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ID YAFA SALTY
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Length 414; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- SUBUNIT: PP2A CONSISTS OF A COMMON HETERODIMERIC CORE ENZYME,
COMPOSED OF A 36 kDa CATALYTIC SUBUNIT (SUBUNIT C) AND A 65 kDa
COMPOSED OF A 36 kDa CATALYTIC SUBUNIT (SUBUNIT ASSOCIATES
WITH A VARIETY OF REGULATORY SUBUNITS. PROTEINS THAT ASSOCIATE
WITH THE CORE DIMER INCLUDE THREE FAMILIES OF REGULATORY SUBUNITS
B (THE R2/F6/F854, R2/F*, '/PR72/PR130/PR59 AND R5/B'/B56
FAMILIES), THE 48 kDa VARIABLE REGULATORY SUBUNIT, VIRAL PROTEINS,
AND CELL SIGNALING MOLECULES.
-1- SUBCELLULAR LOCATION: CYCOPIACM:
-1- PTM: PHOSPHORYLATED ON SERIUR RESIDUES.
-1- SIMILARITY: BELONGS TO THE PHOSPHATASE 2A REGULATORY SUBUNIT B
                                                                                                                                                                                                                                                                                                                                      Zolnierowicz S., van Hoof C., Andjelkovic N., Cron P., Stevens I., Merlevede W., Goris J., Hemmings B.A.; "The variable subunit associated with protein phosphatase 2A0 defines a novel multimember family of regulatory subunits."; Biochem. J. 317:187-194(1996).
  Serine/threonine protein phosphatase 2A, 56 kDa regulatory subunit, epsilon isoform (PP2A, B subunit, B' epsilon isoform) (PP2A, B subunit, B56 epsilon isoform) (PP2A, B subunit, R61 epsilon isoform) (PP2A, B subunit, R78 epsilon isoform).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDINE=96355607; PubMed=8703017; McCright B., Rivers A.M., Audlin S., Virshup D.M.; McCright B., Rivers A.M., Audlin S., Virshup D.M.; "The B56 family of protein phosphatase 2A (PP2A) regulatory subunits encodes differentiation-induced phosphoproteins that target PP2A to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        both nucleus and cytoplasm.";
J. Biol. Chem. 271:22081-22089(1996).
-!- FUNCTION: THE B REGULATORY SUBUNIT MIGHT MODULATE SUBSTRATE SELECTIVITY AND ALSO MIGHT DIRECT THE LOCALIZATION OF THE CATALYTIC ENZYME TO A PARTICULAR SUBCELLULAR
                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 23; DB 1; Length 467; Best Local Similarity 100.0%; Pred. No. 2.5e+02; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               min; Dr. 17. PR. 17. PR. 1856.
Pfam; PF01603; BS6; 1.
Phosphorylation; Multigene family.
SEQUENCE 467 AA; 54699 MW; DD9CE11433F499CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            472 AA.
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND SEQUENCE OF 449-455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                           TISSUE=Fetal retina;
MEDLINE=96276417; PubMed=8694763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z69029; CAA93153.1; -. EMBL; L76703; AAB69752.1; -. Genew; HGNC:9313; PPP2R5E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Fetal brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPARTMENT
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YAPI MOUSE
ID YAPI MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cancer Res. 56:3855-3888(1996).

-!-FUNCTION: THE REGULATORY SUBUNIT MIGHT MODULATE SUBSTRATE
SELECTIVITY AND CATALYTIC SCTIVITY, AND ALSO MIGHT DIRECT THE
LOCALIZATION OF THE CATALYTIC ENZYME TO A PARTICULAR SUBCELLULAR
COMPARIMENT. INTERACTS WITH CYCLIN G IN VITRO.

-!- SUBUNIT: PP2A CONSISTS OF A COMMON HETERODIMERIC CORE ENZYME,
COMPOSED OF A 36 KDA CATALYTIC SUBUNIT (SUBUNIT C) AND A 65 KDA
CONSTANT REGULATORY SUBUNIT (PRES OR SUBUNIT A), THAT ASSOCIATES
WITH A VARIETY OF REGULATORY SUBUNITS. PROTEINS THAT ASSOCIATE
B (THE RZ)AP/RES/BSS, R3/B', PR72/PR130/PRS9 AND RS/B'/BS6
FAMILIES), THE 48 KDA WARLABLE REGULATORY SUBUNIT, VIRAL PROTEINS,
AND CELL SIGNALING MOLECULES.
-!- SUBCELLULAR LOCATION: CYCOPIASMIC (By similarity).
-!- TISSUE SPECIFICITY: HIGHEST LEVELS IN HEART,LIVER AND BRAIN. LOWER
LEVELS IN SKELETAL MUSCLE, SPLEEN, KIDNEY, AND LUNG.
-!- SIMILARITY: BELONGS TO THE PHOSPHATASE 2A REGULATORY SUBUNIT B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                     Tehrani M.A., Mumby M.C., Kamibayashi C., Itahrani M.A., Mumby M.C., Kamibayashi C., Itahrification of a novel protein phosphatase 2A regulatory subunit highly expressed in muscle.";
Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                               STRAIN=CS7BL/6;
MEDLINE=96354596; PubMed=8752144;
Francia_G., Mitchell S.D., Moss S.E., Hanby A.M., Marshall J.F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Identification by differential display of annexin-VI, a gene differentially expressed during melanoma progression."; Cancer Res. 56:1855-1858(1996).
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E3C2DF4C57F729C2 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                        Biol. Chem. 271:5164-5170(1996).
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                                                                                                                                                                                    MEDLINE=96214950; PubMed=8617797;
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                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 15-435 FROM N.A.
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InterPro; IPR002554; B56.
Pfam; PF01603; B56; 1.
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Matches 5; Conserv
                                                                                                                                 SEQUENCE FROM N.A.
                                                                           NCBI_TaxID=10090;
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30-MAY-2000
16-OCT-2001
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ID 2ASE HUMAN
AC Q16537;
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CONFLICT Query Match

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DECARBOXYLASES
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  셤
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                                                                                                                                                                                                                                                                     STRAIN-NIH Swiss; TISSUE-Embryo; MEDLINE-95301570; PubMed=7782338; Sudol M., Bork P., Eibond A., Kastury K., Druck T., Negrini M., Sudol M., Endman D.; Eibond A., Kastury K., Druck T., Negrini M., "Characterization of the mammalian YAP (Yes-associated protein) gene and its role in defining a novel protein module, the WW domain."; J. Blol. Chem. 270:14731-14741(1995).

-I. FUNCTION: BINDS TO THE SH3 DOMAIN OF THE YES KINASE

(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=ST. LAWRENCE 74 / SL 74 / ORS 6A;
MEDLINE=92107187; PubMed=1530878;
Williams L.J., Barnett G.R., Ristow J.L., Pitkin J., Perriere M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes, Sordariales, Sordariaceae, Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 23; DB 1; Length 472; 100.0%; Pred. No. 2.5e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- PTM: PHOSPHORYLATED ON SERINE RESIDUES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50703 MW; 174FD33E0381126C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-EUL-1998 (Rel. 36, Last annotation update)
Ornithine decarboxylase (EC 4.1.1.17) (ODC).
                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   484 AA
              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence upo
15-JUN-2002 (Rel. 41, Last annotation u
65 kDa Yes-associated protein (YAP65).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WW 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X80508; CAA56673.1; -. MGD; MGI:103262; Yap. InterPro; IPR0012349; WW. InterPro; IPR001202; WW_R8P5_WWP. Pfam; PP00397; WW; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS01159; WW_DOMAIN_1; 2. PROSITE; PS50020; WW_DOMAIN_2; 2. Phosphorylation; Repeat.

DOMAIN 215 248 WW 2
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00403; WWDOMAIN.
SMART; SM00456; WW; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                 YAP1 OR YAP65 OR YAP
                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 472 AA;
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neurospora crassa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             450 EILDV 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EILDV 5
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D 227121
DT 01-AUG
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                                                                                                                                                                                                                                                                           -!- PATHWAY: FIRST STEP AND ALSO THE RATE-LIMITING STEP IN THE PATHWAY
Davis R.H.;

"Ornithine decarboxylase gene of Neurospora crassa: isolation,
"Ornithine decarboxylase gene of Neurospora crassa: isolation,
sequence, and polyamine-mediated regulation of its mRNA.";
MOI. Cell. Biol. 12:347-359(1992).
-!- CATALYTIC ACTIVITY: L-ornithine = putrescine + CO(2).
-!- COPACTOR: PYRIDOXAL PHOSPHATE.
-!- COPACTOR: PYRIDOXAL PHOSPHATE.
-!- BY AN EXCESS OF PUTRESCINE. THIS POLYAMINE-MEDIATED CONTROL IS
UNIQUE TO N.CRASSA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-3 IS THE INITIATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McCright B., Virshup D.M.; "Identification of a new family of protein phosphatase 2A regulatory
                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO FAMILY 2 OF ORNITHINE, DAP, AND ARGININE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2ASA_HUMAN STANDARD; PRT; 486 AA.

(015172;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Serine/threonine protein phosphatase 2A, 56 kDa regulatory subunit, alpha isoform (PP2A, B subunit, B' alpha isoform) (PP2A, B subunit, B56 alpha isoform) (PP2A, B subunit, R5 alpha isoform) (PP2A, B subunit, B56 alpha isoform) (PP2A, B subunit, B56 alpha isoform) (PP2A, B subunit, R5 alpha isoform).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO1179; ODBOCRBXIASS.
PROSITE; PS00878; ODB DC 2 1; 1.
PROSITE; PS00879; ODR DC 2 2; 1.
Lyase; Decarboxylase; Pyridoxal phosphate; Polyamine biosynthesis.
BINDING 114 114 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
ACT SITE 422 BY SIMILARITY.
SEQÜENCE 484 AA; 53300 MM; 3554P4315EA44A6F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 23; DB 1; Length 484; 100.0%; Pred. No. 2.6e+02; live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M68969; AAA33604.1; -.
EMBL; M68970; AAA33605.1; -.
EMBL; L16920; AAA33614.1; -.
PIR; A42065; A42065.
HSSP; P07805; A18T.
InterPro; IPR000183; Decarbxy18e2.
Pfam; PP00278; Oxn DAP Arg dec; 1.
Pfam; PF02784; Oxn DAP Arg dec; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Biol. Chem. 270:26123-26128(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96064678; PubMed=7592815;
                                                                                                                                                                                                                                                                                                        POLYAMINE BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 5; Conservative
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(OPRtase); Orotidine 5'-phosphate decarboxylase (EC 4.1.1.23)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              493 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                     NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             271 EILDV 275
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              (OMPdecase)]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2A5B_HUMAN
ID 2A5B_HC
AC Q15173;
DT 30-MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions at long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lab.sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                      SUBUNIT: PPZA CONSISTS OF A COMMON HETERODIMERIC CORE ENZYME, COMPOSED OF A 36 kDa CATALYTIC SUBUNIT (SUBUNIT C) AND A 65 kDa CONSTANT REGULATORY SUBUNIT (PR65 OR SUBUNIT A), THAT ASSOCIATES WITH A VARLETY OF REGULATORY SUBUNITS. PROTEINS THAT ASSOCIATE WITH THE CORE DIMER INCLUDE THREE FAMILIES OF REGULATORY SUBUNITS BY THE CORE DIMER INCLUDE THREE FAMILIES OF REGULATORY SUBUNITS FAMILIES), THE 48 kDa VARIABLE REGULATORY SUBUNITS AND CELL SIGNALING MOLECULES.
                                        Zolnierowicz S., van Hoof C., Andjelkovic N., Cron P., Stevens I., Merlevede W., Goris J., Hemmings B.A.; "The variable subunit associated with protein phosphatase 2A0 defines a novel multimember family of regulatory subunits.";
                                                                                                                                        MEDLINE-95355607; PubMed=8703017;
MCCright B., Rivers A.M., Audlin S., Virshup D.M.;
McCright B. Reduning and cytoplasm.";
J. Biol. Chem. 271:22081-22089(1996)
J. Biol. Chem. 271:22081-22089(1996)
J. Brich McCright McCright Might Modulate Substrate
SELECTIVITY AND CATALYTIC ACTIVITY, AND ALSO MIGHT DIRECT THE
LOCALIZATION OF THE CATALYTIC ENZYME TO A PARTICULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Cytoplasmic.
TISSUE SPECIFICITY: WIDELY EXPRESSED WITH THE HIGHEST EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PYR5_DROME STANDARD; PRT; 493 AA.

Q01637; Q24221;
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Uridine 5'-monophosphate synthase (UMP synthase) (Rudimentary-like protein) [Includes: Orotate phosphoribosyltransferase (EC 2.4.2.10)
                                                                                                                                                                                                                                                                                                                                                                                                                                          PTM: PHOSPHORYLATED ON SERINE RESIDUES.
SIMILARITY: BELONGS TO THE PHOSPHATASE 2A REGULATORY SUBUNIT B
FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E -> F (IN REF. 2; AA SEQUENCE)
H -> S (IN REF. 2; AA SEQUENCE)
R -> E (IN REF. 2; AA SEQUENCE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 23; DB 1; Length 486; 100.0%; Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
 SEQUENCE OF 47-56; 129-132; 347-354; 448-462 AND 471-480
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                                                                                                                                PHOSPHORYLATION, AND SUBCELLULAR LOCATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002554; BS6.
Pfam; PF01603; BS6; 1.
Phosphorylation; Multigene family.
                             MEDLINE=96276417; PubMed=8694763;
                                                                                                                                                                                                                                                                                                                                                                                                                                     IN HEART AND SKELETAL MUSCLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52 52 E
54 54 H
451 451 R
486 AA; 56193 MW;
                                                                                                    Biochem. J. 317:187-194(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L42373; AAC37601.1; -. Genew; HGNC:9309; PPP2R5A.
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54
54
451
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Best Local Similarity
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Bukaryota; Metezao; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Ilsecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                             MEDLINE-91042409; PubMed-2122228;
Bisenberg M.T., Gathy K., Vincent T., Rawls J.;
"Molecular cloning of the UMP synthase gene rudimentary-like from
Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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PROSITE; PS00103; PUR PYR PR TRANSPER; 1.
PROSITE; PS00156; OMPDECASE; 1.
Pyrimidine biosynthesis; Multifunctional enzyme; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 23; DB 1; Length 493; 100.0%; Pred. No. 2.7e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                         SEQUENCE FROM N.A.
Eisenberg M.T., Kirkpatrick R., Rawls J.;
Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REF. 2)
CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGLPQ -> YPDVM (IN
56479CDAB1F6A308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN LINKER. OMPDECASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lyase; Decarboxylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001754; OMPdecase.
InterPro; IPR00836; PRTransferase.
InterPro; IPR002375; Pr/py_rp_transf.
InterPro; IPR004467; PyrE.
Pfam; PF00156; Pribosyltran; 1.
Pfam; PF001515; OMPdecase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _ZASB_HUMAN STANDARD;
Q15173; Q13853;
30-MAY-2000 (Rel. 39, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53327 MW;
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EMBL; X54230; CAA38138.1; -.
PIN; S11907, S11907.
HSSP; P03962; LDQW.
FlyBase; FBGN0003257; r-l.
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Conservative 0
                                                                                                                                                                                                                                                                   SEQUENCE OF 1-78 FROM N.A.
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493
320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!-SUBUNIT: PP2A CONSISTS OF A COMMON HETERODIMERIC CORE ENZYME, COMPOSED OF A 36 KDA CATALYTIC SUBUNIT (SUBUNIT C) AND A 65 KDA COMPOSED OF A 36 KDA CATALYTIC SUBUNIT (SUBUNIT C) AND A 65 KDA CONSTANT REGULATORY SUBUNIT (PR65 OR SUBUNIT A), THAT ASSOCIATES WITH A VARIETY OF REGULATORY SUBUNITS. PROTEINS THAT ASSOCIATE WITH THE CORE DIMER INCLUDE THREE FAMILIES OF REGULATORY SUBUNITS B (THE R2/B/PR55/B55, R3/B''/PR72/PR130/PR59 AND R5/B'/B56 FAMILIES), THE 48 KDB VARIABLE REGULATORY SUBUNIT, VIRAL PROTEINS, AND CELL SIGNALING MOLECULES.
-!- SUBCELLULAR LOCATION: CYCOPIASMIC.
-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; BETA-1 (SHOWN HERE) AND BETA-2; ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN BRAIN.
-!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN BRAIN.
-!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN BRAIN.
-!- THAN AT LEAST ISOFORM BETA-1 IS PHOSPHORYLATED ON SERINE RESIDUES.
-!- PTM: AT LEAST ISOFORM BETA-1 IS PHOSPHATASE, 2A REGULATORY SUBUNIT B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96276417; PubMed=8694763;
Zolnierowicz S., van Hoof C., Andjelkovic N., Cron P., Stevens I.,
Merlevede W., Goris J., Hemmings B.A.;
"The variable subunit associated with protein phosphatase 2A0 defines
a novel multimember family of regulatory subunits.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   both nucleus and cycoplasm.",
J. Biol. Chem. 271.22081-22089(1996).
I- PUNCTION: THE B REGULATORY SUBUNIT MIGHT MODULATE SUBSTRATE
SELECTIVITY AND CATALYTIC ACTIVITY, AND ALSO MIGHT DIRECT THE
LOCALIZATION OF THE CATALYTIC ENZYME TO A PARTICULAR SUBCELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002554; B56.
Pfam; PF01603; B56; 1.
Phosphorylation; Alternative splicing; Multigene family.
VARSPLIC 1 19 METKLPPASTPTSPSSPGL -> MITVNPPLPQDTVNLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHORYLATION, AND SUBCELLULAR LOCATION.
MEDLINE=56355607: Pubmed=8703017;
MCCright B., Rivers A.M., Audlin S., Virshup D.M.;
"The B56 family of protein phosphatase 2A (PP2A) regulatory subunits encodes differentiation-induced phosphoproteins that target PP2A to
                                                                                                                                                                                                                                                                                                                     MEDLINE=56064678; PubMed=7592815;
McCright B., Virshup D.M.;
"Identification of a new family of protein phosphatase 2A regulatory
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Setine/threonine protein phosphatase 2A, 56 KDa regulatory subunit,
beta isoform (PP2A, B subunit, B' beta isoform) (PP2A, B subunit,
B56 beta isoform) (PP2A, B subunit, PR61 beta isoform) (PP2A, B subunit,
subunit, R5 beta isoform).
                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleogtomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM BETA-2), AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                     Biol. Chem. 270:26123-26128(1995).
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM BETA-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L42374; AAC37602.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Z69028; CAA93152.1;
HGNC:9310; PPP2R5B
                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                          rISSUE=Fetal brain;
                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPARTMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rissum-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM; 601644;
                                                                                                                                                                                                                                                                                                                                                                                                  subunits."
                                                                                                                                            PPP2R5B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
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                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Depaoli-Roach A.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBUNIT: PP2A CONSISTS OF A COMMON HETERODIMERIC CORE ENZYME,
COMPOSED OF A 36 kDa CATALYTIC SUBUNIT (SUBUNIT C) AND A 65 kDa
CONSTANT REGULATORY SUBUNIT (PR65 or SUBUNIT A), THAT ASSOCIATES
WITH A VARIETY OF REGULATORY SUBUNITS. PROTEINS THAT ASSOCIATE
B THE R.2/B/PR55/B55, R3/B*, 'PR72/PR130/PR59 AND R5/B*/B56
FAMILIES), THE 48 kDa VARIABLE REGULATORY SUBUNIT; VIRAL PROTEINS,
AND CELL SIGNALING MOLECULES.
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN.
-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              isoforms.";
J. Biol. Chem. 271:2578-2588(1996).

-!- FUNCTION: THE B REGULATORY SUBUNIT MIGHT MODULATE SUBSTRATE
-!- FUNCTION: THE B REGULATORY SUBUNIT MIGHT MODULATE SELECTIVITY AND ALSO MIGHT DIRECT THE
LOCALIZATION OF THE CATALYTIC ENZYME TO A PARTICULAR SUBGELLULAR
                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Serine/threonine protein phosphatase 2A, 56 kDa regulatory subunit,
Berine/threonine protein phosphatase 2A, 56 kDa regulatory subunit,
Beta isoform (PP2A, B subunit, B' beta isoform) (PP2A, B subunit,
B56 beta isoform) (PP2A, B subunit, PR61 beta isoform) (PP2A, B
subunit, R5 beta isoform) (PP2A, B subunit, B'-alpha).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96161994; PubMed=8576224;
Csortcs C., Zolnierowicz S., Bako B., Durbin S.D., Depaoli-Roach A.)
"High complexity in the expression of the B' subunit of protein
phosphatase 2A0. Evidence for the existence of at least seven novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryotas, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAUTION: NOMENCLATURE USED IN REF.1 REFERS TO PP2A B SUBUNIT B' ALPHA ISOFORM, WHICH IS CITED AS PP2A B SUBUNIT BETA-PR61 ISOFORM IN LATER PUBLICATIONS.
(IN ISOFORM BETA-2).
QB -> IF (IN REF. 2; AA SEQUENCE).
ES -> GA (IN REF. 2; AA SEQUENCE).
F -> M (IN REF. 2; AA SEQUENCE).
S -> M (IN REF. 2; AA SEQUENCE).
W -> E (IN REF. 2; AA SEQUENCE).
W -> E (IN REF. 2; AA SEQUENCE).
                                                                                                                                                                                    ö
                                                                                                                                               Length 497;
                                                                                                                                Score 23; DB 1; Length 4>
Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                      500 AA
                                                                                                                                                                                     0; Mismatches
                   58 QE
178 ES
181 F
184 S
461 W
57393 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryctolagus cuniculus (Rabbit)
                                                                                                                                                 100.0%;
                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                     57
177
181
184
461
497 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=New Zealand;
                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPARTMENT
                                                                                                                                                                                                                                                            341 EILDV 345
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                                                                                                                                                                                                                                                                                                                                                  2A5B RABIT
Q28647;
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2
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                   CONFLICT
CONFLICT
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SEQUENCE
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                                                                                                                                                                                     Matches
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EMBL, U37769, AAC48527.1; -. InterPro, IPR002554; B56. Pfam; PF01603; B56; 1.

Matches

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                                                                                                                                                                                                                                                                                                                       "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.";
Science 286:1571-1577(1999)
-!- CATALYTIC ACTIVITY: ATP + glycine + tRNA(Gly) = AMP + diphosphate + glycyl-tRNA(Gly).
-!- SUBGUNIT: HOMODIMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGRFAMS; TIGR00389; GlyS dimeric; 1.
PROSITE; PSS0862; AA TRNA_LIGASE II; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                    MEDLINE=20036896; PubMed=10567266;
White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
 16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Glycyl-tRNA synthetase (EC 6.1.1.14) (Glycine--tRNA ligase) (GlyRS).
GLYS OR DR2059.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Canis familiaris (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Pissipedia, Canidae, Canis.
                                                                                 Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 23; DB 1; Length 506; 100.0%; Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              506 AA; 57204 MW; 23A7C69DE83D2D01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FINC_CANFA STANDARD; PRT; 522 AA. Q28275; Q28276; D1-NOV-1997 (Rel. 35, Created) 1-NOV-1997 (Rel. 35, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Fibronectin (FN) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001106; AAtRNA_ligaseII.
InterPro; IPR004154; HGYP anticodon.
InterPro; IPR002314; tRNA-synt_2b.
InterPro; IPR002315; tRNA-synt_gly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE002042; AAF11606.1; ALT_INIT.
HSSP; P56206; 1ATI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00587; tRNA-synt 2b; 1.
Pfam; PF03129; HGTP anticodon; 1.
PRINTS; PR01043; TRNASYNTHGLY.
                                                                                                      Deinococcaceae; Deinococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                 Deinococcus radiodurans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 5; Conserv
                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                          NCBI_TaxID=1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rigk; DR2059; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                276 EILDV 280
                                                                                                                                                                                                                                                                                                             Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EILDV 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 44
FINC CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- CATALYTIC ACTIVITY: ATP + glycerol = ADP + glycerol 3-phosphate.
-!- PATHWAY: Glycerol utilization; rate-limiting step.
-!- SIMILARITY: BELONGS TO THE FUCOKINASE / GLUCONOKINASE / GLYCEROKINASE / XYLULOKINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: KEY ENZYME IN THE REGULATION OF GLYCEROL UPTAKE AND METABOLISM.
                                                                                                                                                                                                                                                                      30-MX-2000 (Rel. 39, Created)
30-MX-2000 (Rel. 39, Last sequence update)
15-UNA-2002 (Rel. 41, Last annotation update)
Glycerol kinase (EC 2.7.1.30) (ATF:glycerol 3-phosphotransferase)
(Glycerokinase) (GK).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas tolaasii.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                   Length 500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 23; DB 1; Length 503; 100.0%; Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 23; DB 1; Length 50
100.0%; Pred. No. 2.7e+02;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
Multigene family; Nuclear protein.
SEQUENCE 500 AA; 57709 MW; 001CA9360E4C04B0 CRC64;
                                                                                                                                                                                                                                             503 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          506 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murata H.;
"GlpK of Pseudomonas tolaasii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 43
SYG_DEIRA
ID SYG_DEIRA STANDARD;
1AC OPRER5;
DT 16-OCT-2001 (Rel. 40, Created)
                                                                 Local Similarity 100.
nes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.
                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas.
NCBI_TaxID=29442;
                                                                                                                                                      341 EILDV 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   211 EİLDV 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=PT814;
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                                                                                                                      1 EILDV
                                                                                                                                                                                                                                        GLPK PSETO
087924;
                                                   Query Match
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Gaps

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Matches

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MEDLINE-96324981; PubMed=8702559;
MEDLINE-96324981; PubMed=8702559;
MEDLINE-96324981; PubMed=8702559;
MEDLINE-96324981; PubMed=8702559;
MEDLINE-96324981; PubMed=8702559;
MEDLINE-96324981; PubMed=8702559;
MEDLINE-96324981; PubMed=8702559;
MEDLINE-96324981; PubMed=8702559;
MEDLINE-96324981; PubMed=8702559;
MEDLINE-96324981; PubMed=8701496;
MEDLING COLLAGEN; FIBRIN, HEPARIN, DNA, AND ACTIN. FIBRONECTINS ARE INVOLVED IN CELL ADHESION, CELL MOTILITY, OFSONIZATION, WOUND HEALING, AND MAINTENANCE OF CELL SHAPE.
MEALING, AND MAINTENANCE OF CELL MOTILITY, OFSONIZATION, WOUND HEALING, AND MAINTENANCE OF CALL MOTILITY, OFSONIZATION, WOUND HEALING, AND MAINTENANCE OF CALL MOTILIERS OF ALTERNATIVE SPLICED VALIANTS, CONNECTED BY 2 DISGLIFINE BONDS NEAR THE CARBOXYL ENDS;
MALERNATIVE PRODUCTS: BACH OF FIRENOBECTIN TYPE-11, REPEAT 10 OF FIRENOBECTIN TYPE-11, REPEAT 10 OF FIRENOBECTIN TYPE-11, REPEAT 10 OF FIRENOBECTIN TYPE-11, AND THE CONNECTING STRAND 3.

MALE STREAM FOR THE MAJOR FRANSCRIPT IN PRIMERIC OR CROSS-LINKED MULTIMERIC FORM); MADE BY FIRENOBLASTS, EPITHELIAL AND OTHER CELL TYPES, IS DEPOSITED AS FIRENILS IN THE EXTRACELLULAR MATRIX, VARIANT (V+C)-CONNECTIVE DEPOSITED AS FIRENILS IN THE EXTRACELLULAR MATRIX. SARENT THE CONNECTIVE PRODUCTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lab-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HEPARIN-BINDING 2 (BY SIMILARITY).
FIBRING-BINDING 2 (BY SIMILARITY).
FIBRONECTIN TYPE-111 14.
FIBRONECTIN TYPE-111 14.
FIBRONECTIN TYPE-111 16.
FIBRONECTIN TYPE-111 16.
FIBRONECTIN TYPE-1 11.
FIBRONECTIN TYPE-1 10.
FIBRONECTIN TYPE-1 11.
FIBRONECTIN TYPE-1 11.
FIBRONECTIN TYPE-1 11.
FIBRONECTIN TYPE-1 11.
FIBRONECTIN TYPE-1 12.
CELL ATTACHMENT SITE (POTENTIAL).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, US2106; AAC48612.1; --
EMBL, US2106; AAC48611.1; --
HSSP; PO2751; IFNH.
INTERPRO'S IPRO03961; FN III.
INTERPRO'S IPRO0083; FIDERCINI.
PERM, PPO0041; fn1; 3.
PERM, PF00041; fn1; 3.
SWART; SW00069; FN1; 2.
SWART; SW00069; FN3; 3.
GLYCOPICATE; PS01253; FIBRONECTIN 1; 2.
GLYCOPICATE; PASSMAN HEPARIN-binding; Acute phase; Cell adhesion; Novement. Sulfation; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTM: SULFATED (BY SIMILARITY).
SIMILARITY: CONTAINS AT LEAST 4 FIBRONECTIN TYPE III DOMAINS.
SIMILARITY: CONTAINS AT LEAST 3 FIBRONECTIN TYPE I DOMAINS.
                              SEQUENCE FROM N.A., AND VARIANT (V+C) -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FROM LIVER.
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CARBOHYD
VARSPLIC
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RA MEDLINES-95.74943; PURDEGRAG VIOLED ST.

RA MEDLINES-95.74943; PURDEGRAG VIOLED ST.

RET GROGING THE V. III-15, and I-10 protein segments.";

RI SHOLOCATION RNA splice variant in articular cartilage lacks bases encoding the V. III-15, and I-10 protein segments.";

RI GROGING THE V. III-15, and I-10 protein segments.";

RI J. Biol Chem. 271.18954-18960[1996].

CC -1- FUNCTION: PIBRONECTINS BIND CELL SURFACES AND VARIOUS COMPOUNDS

CC -1- FUNCTION: PIBRONECTIN BIND CELL SHAPE.

CC -1- FUNCTION: VARIANT (V+C)- IS PROBABLY INVOLVED IN MATRIX

ORGANIZATION OF CARTILAGE.

CC -1- SUBDNITS MOSTLY HETERODIMERS OR MULTIMERS OF ALTERNATIVE SPLICED

VARIANTS, CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS;

CC -1- SUBDNITS CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS;

CC -1- ALTERNATIVE PRODUCTS: EACH OF THE "EXTRA DOMAIN" & THE CONNECTING STRAND 3 ARE PRESENT IN SOME FORMS OF PIBRONECTIN AND ABSENT IN CV+C)- LACKS REPERAT 15 OF PIBRONECTIN TYPE-111, REPEAT 10 OF FIBRONECTIN TYPE-111, AND THE CONNECTING STRAND 3.

CC -1- TISSUE SPECIFICITY: PLASMA FN (SOLUBLE DIMERIC FORM) IN EXPERSION OF FIBRONECTIN TYPE-111, AND THE CONNECTING STRAND 3.

CC -1- TISSUE SPECIFICITY: PLASMA FN (SOLUBLE DIMERIC FORM), MADE BY FIBROHEASTS, RETHALLIAL AND OTHER CELL TYPES, IS CORNS), MADE BY FIBROHEASTS, RETHALLIAR MADOR TRANSCRIPT IN ARTICULAR CARTIAGE, VERY LOW LEVELS IN LYMPH NODE, BONE, AORTA, AND SKIN; ABSENT FROM LIVER, SPLEEN, CC INTERNATIVE, AND TRANSCRIPT IN ARTICULAR CARTIAGE, VERY LOW LEVELS IN LIVERH NODE, BONE, AORTA, AND SKIN; ABSENT FROM LIVER, SPLEEN, CC INTERNATIVE, AND THE CONTAINS.

CC -1- TISSUE SPECIFICITY: PLASMA FN (SOLUBLE DIMERIC FORM).

CC -1- TISSUE SPECIFICITY: PLASMA FN (DIMERIC STRAND CONTAINS, AND STRAND ABSENT THE CONTAINS AT LEAST 4 FIBRONECTIN TYPE IID DOMAINS.

CC -1- TISSUE SPECIFICITY.

CC -1- TISSUE SPECIFICITY.

CC -1- TISSUE SPECIFICITY.

CC -1- TISSUE SPECIFICITY: PLASMA FN (DIMERIC STRAND CONTAINS).

CC -1- TISSUE SPECIFICITY: PLASMA FN (DIMERIC STRAND CONTAINS).

CC -1- TISSUE SPEC
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                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eguus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Eguus.
                                                                                                                                                                                                                                          ö
                                                                                                                                                             Length 522;
        MISSING (IN ISOFORM (V+C)-).
                                                                                                                                                                                                                                          0; Indels
                                                                                57700 MW; DB1D9A54C2BDAE26 CRC64;
                                                                                                                                                         Score 23; DB 1; I
Pred. No. 2.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-CCT-2001 (Rel. 40, Last annotation update)
Fibronectin (FN) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 522 AA
                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96324983; PubMed=8702559;
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InterPro; IPR000083; Fibrnctn1
                                                                                                                                                             100.0%;
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                                                                                                                                                                                                                                          5; Conservative
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206 4
522 5
522 AA;
                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                           222 EILDV 226
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VARSPLIC
NON TER
SEQUENCE
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VARSPLIC
CONFLICT
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"The variable subunit associated with protein phosphatase 2A0 defines a novel multimember family of regulatory subunits.";
Biochem. J. 317:187-194(1996).
                                                                                                                                                   FIRENCE CONTRIBUTION OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF THE STATEMENT OF
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rīdentification of a novel protein phosphatase 2A regulatory subunit
iqhlv expressed in musche ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2ASG HUMAN STANDARD; PRT; 524 AA.

Q13362; Q14391; Q15174; Q15060;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Serinef threonine protein phosphatase 2A, 56 kDa regulatory subunit, gamma isoform (PP2A, B subunit, B' gamma isoform) (PP2A, B subunit, B' gamma isoform) (PP2A, B subunit, RS gamma isoform).
Pfam; PF00039; fn1; 3.
Pfam; PF00041; fn3; 3.
SMART; SM0058; FN1; 2.
SMART; SW00060; FN3; 3.
PR03TE; PS01253; FIBRONECTIN 1; 2.
Glycoprotein; Plasma; Heparin-binding; Acute phase; Cell adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                        HEPARIN-BINDING 2 (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 522;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 23; DB 1; I
100.0%; Pred. No. 2.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                Repeat; Sulfation; Alternative splicing.
NON TER 1 204 HEPARIN-ETN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           highly expressed in muscle.";
J. Biol. Chem. 271:5164-5170(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Umbilical vein;
MEDLINE=96214950; PubMed=8617797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Fetal retina;
MEDLINE=96276417; PubMed=8694763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Conservative
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491
501
321
205
462
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522 AA;
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Best Local Similarity
Matches 5; Conserv
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THE AT LEAAT ISOPORM GAMMA-3 IS PHOSPHORYLATED ON SERINE RESIDUES WHILE ISOPORM GAMMA-1 IS NOT.
SIMILARITY: BELONGS TO THE PHOSPHATASE 2A REGULATORY SUBUNIT B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
YTVYSQASTWSIPVAMETDGPLFEDVQMLRKTVKDEAHQAQ
KDPKKDRPLALRKSELPQDPHTKKALBAHCRADELASQDGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i-SUBUNIT: PP2A CONSISTS OF A COMMON HETERODIMERIC CORE ENZYME,
COMPOSED OF A 36 kDa CATALYTIC SUBUNIT (SUBUNIT S), THAT ASSOCIATES
CONSTANT REGULATORY SUBUNIT (PR65 OR SUBUNIT A), THAT ASSOCIATES
WITH A VARIETY OF REGULATORY SUBUNITS. PROTEINS THAT ASSOCIATE
WITH THE CORE DIMER INCLUDE THREE FAMILIES OF REGULATORY SUBUNITS
B (THE R2/B/PR55/B55, R3/B'', PR72/PR130/PR59 AND R5/B'/B56
FAMILIES), THE 48 kDa VARIABLE REGULATORY SUBUNIT, VIRAL PROTEINS,
AND CELL SIGNALING MOLECULES.
-I-SUBCELLULAR LOCATION: Nuclear (isoforms 1 and 3).
-I-SUBCELLULAR ENDUCTS: 3 ISOFORMS, GAMMA-2 AND GAMMA-3
(SHOWN HERE), ARE PRODUCED BY ALTERNATIVE SPLICING.
-I-TISSUE SPECIFICITY: HIGHEST LEVELS IN HEART, SKELETAL MUSCLE AND
BRAIN: LOWER LEVELS IN PANCREAS, KIDNEY, LUNG AND PLACENTA. VERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96355607; PubMed=8703017;
MCCTIGHT B., Rivers A.M., Audlin S., Virshup D.M.;
MCTIGHT B. Early of protein phosphatase 2A (PP2A) regulatory subunits encodes differentiation-induced phosphoproteins that target PP2A to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   both nucleus and cytoplasm.";
J. Biol. Chem. 271:22081-22089(1996).
-!- FUNCTION: THE B REGULATORY SUBUNIT MIGHT MODULATE SUBSTRATE SELECTIVITY AND ALSO MIGHT DIRECT THE LOCALIZATION OF THE CATALYTIC ENZYME TO A PARTICULAR SUBCELLULAR
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 11-524 FROM N.A. (ISOFORM GAMMA-1).
MEDLINE=96064678; PubMed=1592815;
MCCTight B., Virsh PubMed | MCCTight B., Virsh D.M.;
"Identification of a new family of protein phosphatase 2A regulatory
TISSUE=Bone marrow;

MEDLINE=86051398; PubMed=7584044;

MEDLINE=86051398; PubMed=7584044;

Seki N., Nagaee T., Miyajima N., Sazuka T., Tanaka A., Sato S.,
Seki N., Kawarabayasi Y., Ishikawa K.-I., Tabata S.;

"Prediction of the coding sequences of unidentified human genes. II.
The coding sequences of 40 new genes (KIAA0081-KIAA0080) deduced by
analysis of cDNA clones from human cell line KG-I.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -> VLKKRIT (IN ISÖFORM GAMMA-1).
MISSING (IN ISOFORM GAMMA-2).
L -> R (IN REF. 3).
28EBF54550D70C19 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002554; B56.
Pfam; PF01603; B56; 1.
Nuclear protein; Phosphorylation; Alternative splicing;
Multigene family.
DOMAIN 416 422 NUCLEAR LOCALIZATION CICHNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHORYLATION, AND SUBCELLULAR LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biol. Chem. 270:26123-26128(1995).
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EMBL, Z69303, CAA93154.1; -
EMBL, D26445; BAA03465.1; -
EMBL, L42375; AAC37603.1; -
Genew, HGNC:9311; PPP2R5C.
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                                                                                                                                                                                                                                                                                         DNA Res. 1:223-229(1994).
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524
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494 4
524 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                subunits."
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Length 524;

DB 1;

Score 23;

100.08;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alternative splicing; Multigene family; Nuclear protein.
DOMAIN
A72 489 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
VARSPLIC 482 524 AQKOPKKERPLARRKSELPODPHTKKALEAHCRADELVPOD
GR -> QLVGRKAVSSTQVRKV (IN ISOFORM GAMMA-4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=New Zealand; TISSUE=Skeletal muscle;
MEDLINE=96161994; PubMed=8576224;
CSOTTOS C., Zolnierowicz S., Bako E., Durbin S.D., Depaoli-Roach A.A.;
"High complexity in the expression of the B' subunit of protein phosphatase 2A0. Evidence for the existence of at least seven novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Nuclear (By similarity).
ALTERNATIVE PRODUCTS: 4 ISOFORMS; GAMMA-1/BETA-4, GAMMA-3/BETA-3 (SHOWN HERE), GAMMA-4/BETA-1 AND GAMMA-5/BETA-2; ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: PP2A CONSISTS OF A COMMON HETERODIMERIC CORE ENZYME, COMPOSED OF A 36 kDa CATALYTIC SUBUNIT (SUBUNIT C) AND A 65 kDa CONSTANT REGULATORY SUBUNIT (PR65 OR SUBUNIT A), THAT ASSOCIATES WITH A VARLETY OF REGULATORY SUBUNITS. PROTEINS THAT ASSOCIATE WITH THE CORE DIMER INCLUDE THREE FAMILIES OF REGULATORY SUBUNITS BY THE CORE DIMER INCLUDE THREE FAMILIES OF REGULATORY SUBUNITS FAMILIES), THE 48 kDa VARIABLE REGULATORY SUBUNITS AND CELL SIGNALING MOLECULES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTIS, HEART AND SPLEEN. ALSO FOUND IN BRAIN AND SKELETAL MUSCLE. SIMILARITY: BELONGS TO THE PHOSPHATASE 2A REGULATORY SUBUNIT B
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1:01. Chem. 271:2578-2588(1996).
FUNCTION: THE B REGULATORY SUBUNIT MIGHT MODULATE SUBSTRATE
SELECTIVITY AND CAPLYTIC ACTIVITY, AND ALSO MIGHT DIRECT THE
LOCALIZATION OF THE CATALYTIC ENZYME TO A PARTICULAR SUBCELLULAR
                                                                                                                                                                                                                                            Q28651; Q28648; Q28652; Q28651; Q286551; Q28648; Q28651; Q28651; Q286551; Q286551; Q286551; Q286551; Q28650; Q28650; Q28650; Q29.MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
Serine/threonine protein phosphatase 2A, 56 kDa regulatory subunit, gamma isoform (PP2A, B subunit, BY gamma isoform) (PP2A, B subunit, BF61 gamma isoform) (PP2A, B subunit, Rel gamma isoform) (PP2A, B subunit, BY beta isoform)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                     ö
                                     0; Indels
             Pred. No. 2.8e+02;
Mismatches 0;
                                                                                                                                                                                                                                 524 AA
100.08; Pre-
                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryctolagus cuniculus (Rabbit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U38191; AAC48530.1; -. EMBL; U37770; AAC48528.1; -. EMBL; U38190; AAC48529.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U38192; AAC48531.1; -. InterPro; IPR002554; B56.
Pfam; PF01603; B56; 1.
                                     Conservative
               Best Local Similarity
Matches 5, Conserv
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                                                                           1 EILDV 5
                                                                                                                                                                                                                                 2A5G RABIT
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AQKOPKKERPLARRKSELPQDPHTKKALEAHCRADELVPQD
GR -> VKVPG (IN ISOPORM GAMMA -5)
YSCSHASTVSMPLAMETDGPLFBDVMLRKTVSDEARQAQ
YDPKKERPLARRKSELPQDPHTKKALEAHCRADELVPQDGR
-> VLKKRAI (IN ISOPORM GAMMA-1)
DC4520D122DAP386 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey B.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., LeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Eisen J., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TENA (FMET) AMINOACYLATION.
-!- CATALYTIC ACTIVITY: ATP + L-methionine + tRNA (Met) = AMP + diphosphate + L-methionyl-tRNA (Met).
-!- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
-!- SUBGELIUAR LOCATION: CYFOPLASMIC.
-!- SIMILARITY: BELONGS TO CLASS-1 AMINOACYL-TRNA SYNTHETASE FAMILY.
STRONG, TO CYSTEINYL-TRNA SYNTHETASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shirai M., Hirakwa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; Couchi K., Hattori M., Kuhara S., Nakazawa T.; Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CW1029 from USA.", Nucleic Acids Res. 28:2311-2314(2000).

-I-PUNCTION: IT IS PROBABLY ESSENTIAL FOR CELL SURVIVAL, BEING REQUIRED NOT ONLY FOR ELONGATION OF PROTEIN SYNTHESIS BUT ALSO FOR THE INITIATION OF ALL MRNA TRANSLATION THROUGH INITIATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CWL029;
MICHOLINE=99206606; PubMed=10192388;
Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
"Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
Nat. Genet. 21:385-389(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYM CHLPN STANDARD; PRT; 551 AA.
09255; 090RW1;
30-MAY-2000 (Rel. 39, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Methionyl-tRNA synthetase (EC 6.1.1.10) (Methionine--tRNA ligase)
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                                                                                                                                                                                                                                    Length 524;
                                                                                                                                                                                                                                                                                                  IndelB
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila
NCBI_TaxID=83558;
                                                                                                                                                                                                                                 100.0%; Score 23; DB 1; L. L. L. L. L. 100.0%; Pred. No. 2.8e+02; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000)
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                                                                                                                                                                   60984 MW;
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les 5; Conserv
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      482
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          VARSPLIC
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Matches
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Homo sapiens (Human)
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2ASD_HUMAN
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN-New Zealand; TISSUE-Brain, and Skeletal muscle;
MRDLINE-96161994; PubMed-8576224;
CROINE-967. Zolnierowicz S., Bako E., Durbin S.D., Depaoli-Roach A.A.;
"High complexity in the expression of the B' subunit of protein phosphatase 2A0. Evidence for the existence of at least seven novel
                                                                                                                                                                                                                                                                                     Pfam; PF00133; tRNA-synt 1; 1.—PRINTS; PR0141; TRNA-SYNTHMET.
TIGRFAMS; TIGR00398; metG; 1.
PROSITE; PS00178; AA TRNA_TGNET.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding; Metal-binding; Zinc; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biol. Chem. 271:2578-2588 (1996).
- FUNCTION: THE B REGULATORY SUBUNIT MIGHT MODULATE SUBSTRATE SELECTIVITY AND CATALYTIC ACTIVITY, AND ALSO MIGHT DIRECT THE LOCALIZATION OF THE CATALYTIC ENZYME TO A PARTICULAR SUBCELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: PP2A CONSISTS OF A COMMON HETERODIMERIC CORE ENZYME, COMPOSED OF A 36 KDA CATALYTIC SUBUNIT (SUBUNIT C) AND A 65 KDA CONSTANT REGULATORY SUBUNIT (PR65 or SUBUNIT A), THAT ASSOCIATES WITH A VARIETY OF REGULATORY SUBUNITS. PROTEINS THAT ASSOCIATE
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subunit,
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30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
25-fine(hirconine protein phosphatase 24, 56 kDa regulatory subunit delta isoform (PP2A, B subunit, B' delta isoform) (PP2A, B subunit, B56 delta isoform) (PP2A, B subunit, PR61 delta isoform) (PP2A, B subunit, R61 delta isoform) (PP2A, B subunit, R61 delta isoform) (PP2A, B subunit, R61 delta isoform) (PP2A, B subunit, B61 delta isoform)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 23; DB 1; Length 551; 100.0%; Pred. No. 3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAB2E383314E2B19 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                             "HIGH" REGION.
"KMSKS" REGION.
ATP (BY SIMILARITY).
ZINC (BY SIMILARITY).
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V -> A (IN REF. 1).
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InterPro; IPR001412; tRNA-synt I.
InterPro; IPR002304; tRNA-synt met.
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                                                                                                  EMBL, AE001598; AAD18275.1; -. EMBL, AE002223; AAF38466.1; -. EMBL, AP002545; BAA98333.1; -. HSSP; P00959; 1MEA.
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PHCI-2DPAGE; Q9Z959; -.
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551 AA;
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                                                                                                                                                                                                      TIGR; CP0651;
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2ASD RASDIT
2ASD RASDIT
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WITH THE CORE DIMER INCLUDE THREE FAMILIES OF REGULATORY SUBUNITS
B (THE R2/B/PR55/B55, R3/B''/PR72/PR130/PR59 AND R5/B'/B56
FAMILIES), THE 48 KDA VARIABLE REGULATORY SUBUNIT, VIRAL PROTEINS,
AND CELL SIGNALING MOLECULES (By similarity).
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN.
-!- SIMILARITY: BELONGS TO THE PHOSPHATASE 2A REGULATORY SUBUNIT B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SH3 BINDING, CLASS I (POTENTIAL).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
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that target PP2A to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Multigene family, Nuclear protein, Repeat.
DOMAIN 21 36 8 X 2 AA APPROXIMATE TANDEM REPEATS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DASD HUMAN STANDARD; PRT; 602 AA.

Q14736; O00696; O00494; Q15171;
30-MAY-2000 (Rel. 39, Created)
15-JUN-2002 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
Serine/threonine protein phosphatese 2A, 56 kDa regulatory subunit,
delta isoform (PPZA, B subunit, B' delta isoform) (PPZA, B subunit,
B56 delta isoform) (PPZA, B subunit, PR61 delta isoform) (PPZA, B subunit,
subunit, R5 delta isoform).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Brain cortex;
MEDLINE=97324098; PubMed=9180267;
Tanabe O., Gomez G.A., Niahito Y., Usui H., Takeda M.;
"Molecular heterogeneity of the cDNA encoding a 74-kDa regulatory subunit (B'' or delta) of human protein phosphatase 2A.";
FEBS Lett. 408:52-56(1997).
                                                                                                                                                                                                                                                                                                                                           CAUTION: NOMENCLATURE USED IN REF.1 REFERS TO PP2A B SUBUNIT B' GAMMA ISOFORM, WHICH IS CITED AS PP2A B SUBUNIT DELTA-PR61 ISOFORM IN LATER PUBLICATIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68090 MW; E149A309CDDA7495 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM DELTA-1).

TISSUE=Fetal brain;

MEDLINE=96355607; PubMed=8703017;

MCLIGHT B., Rivers A.M., Audlin S., Virshup D.M.;

"The B56 family of protein phosphatase 2A (PP2A) reguencodes differentiation-induced phosphoproteins that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORMS DELTA-1 AND DELTA-3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             both nucleus and cytoplasm.";
J. Biol. Chem. 271:22081-22089(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U38193; AAC48532.1; -. EMBL; U38195; AAC48534.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002554; B56.
Pfam; PF01603; B56; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBBUNIT: PP2A CONSISTS OF A COMMON HETERODIMERIC CORE ENZYME,
COMPOSED OF A 36 kDa CATALYTIC SUBUNIT (SUBUNIT C) AND A 65 kDa
CONSTANT REGULATORY SUBUNIT (PR65 OR SUBUNIT A), THAT ASSOCIATES
WITH A VARIETY OF REGULATORY SUBUNITS. PROTEINS THAT ASSOCIATE
WITH THE CORE DIMER INCLUDE THREE FAMILIES OF REGULATORY SUBUNITS
B (THE R2/B/PR55/B55, R3/B''/PR72/PR130/PR59 AND R5/B'/B56
FAMILIES), THE 48 kDa VARIABLE REGULATORY SUBUNIT, VIRAL PROTEINS,
AND CELL SIGNALING MOLECULES.
SUBGELJULAR LOCATION: CYTOPLASMIC AND NUCLEAR IN INTERPHASE,
NUCLEAR DURING MITOSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.; Substraint of the EMBL/GenBank/DDBJ databases. Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. -!- PUNCTION: THE B REGULATORY SUBMIT MIGHT MODULATE SIBLECTIVITY AND CATALYTIC ACTIVITY, AND ALSO MIGHT DIRECT THE LOCALIZATION OF THE CATALYTIC ENZYME TO A PARTICULAR SUBCELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALTERNATIVE PRODUCTS: 3 ISOFORMS; DELTA-1 (SHOWN HERE), DELTA-2
AND DELTA-3; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: ISOFORM DELTA-2 IS WIDELY EXPRESSED. ISOFORM
DELTA-1 IS HIGHLY EXPRESSED IN BEARA.
INDUCTION: BY RETINOIC ACID; IN NEUROBLASTOMA CELL LINES.
PTM: AT LEAST ISOFORM DELTA-1 IS PHOSPHORYLATED ON SERINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SH3 BINDING, CLASS I (POTENTIAL).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
MISSING (IN ISOFORM DELTA-3).
MISSING (IN ISOFORM DELTA-2).
                                                                                                                     Hayashi H., Ragamiyama H., Takeda M.;
"Molecular cloning of a 74-kDa regulatory subunit (B'' or delta) of human protein phosphatase 2A.";
FEBS Lett. 379:107-111(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 X 2 AA APPROXIMATE TANDEM REPEATS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE PHOSPHATASE 2A REGULATORY SUBUNIT B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nuclear protein; Phosphorylation; Alternative splicing; Repeat; Multigene family.
                           SEQUENCE FROM N.A. (ISOFORM DELTA-2), AND SEQUENCE OF 501-508; 550-559; 573-580 AND 584-601 (DELTA-1).
TISSUE-Brain cortex, and Bone marrow;
MEDLINE-86159032; PubMed-8566219;
Tanabe O., Nagase T., Murakami T., Nozaki H., Usui H., Nishito
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F15F71AF4E565387 CRC64;
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORMS DELTA-1 AND DELTA-2) TISSUE-Colon, Eye, and Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; BC001095; AAH01095.1; -.
EMBL; BC001175; AAH01175.1; -.
EMBL; BC010692; AAH10692.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L76702; AAB69751.1; -.
EMBL; AB000634; BAA20381.1; -.
EMBL; AB000635; BAA20382.1; -.
EMBL; D78360; BAA11372.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 116 M
85 116 M
602 AA; 6991 MW;
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Pfam; PF01603; B56; 1.
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SEQUENCE
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                 halodurans and genomic sequence comparison with Bacillus subtilis.";

Nucleic Acids Res. 28:4317-4331(2000).

-- FUNCTION: THE REACTION CATALYZED BY TOPOISOMERASES LEADS TO THE CONVERSION OF OWER TOPOLOGICAL ISOMER OF DNA TO ANOTHER.

-- CATALYTIC ACTIVITY: ATP-independent breakage of single-stranded DNA, followed by passage and rejoining.

-- SUBUNI: MONOMER (BY SIMILARITY).

-- MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA BACKBONE BOND, IT SIMULARITYD.

WHICH A TYROSYL OXYGEN IN THE SEXTME IS JOINED TO A DNA PHOSPHORUS AT ONE END OF THE ENZYME-SEVERED DNA STRAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA topoisomerase I (EC 5.99.1.2) (Omega-protein) (Relaxing enzyme)
(Untwisting enzyme) (Swivelase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TICRFAMS; TICR01051; topA bact; 1.
PROSITE; PS00396; TOPOISOMERASE I PROK; 1.
Isomerase; Topoisomerase; DNA-binding; Zinc-finger; Metal-binding;
                                                                                                                                                                                                                                                                                                            Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence of the alkaliphilic bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOISOMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA CLEAVAGE (BY SIMILARITY).
                                                                                                                                                                               Bacillus halodurans.
Bacteria, Firmicutes; Bacillales; Bacillaceae, Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EE3E9EE0B5546256 CRC64;
                                    690 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002936; DNAprim toprim.
InterPro; IPR002936; DNAtopI_ATP bind.
InterPro; IPR003802; DNAtopI_DNA_Dind.
InterPro; IPR0003802; DNAtopI_DNA_Dind.
InterPro; IPR0003802; DNAtopI_DNA_Dind.
InterPro; IPR0003802; DNAtopIII; Topoisom_bac; 1.
PEam; PP01191; Topoisom_bac; 1.
PRINTS; PR00417; PRTPISMRASEI.
SWART; SM00493; TOPIBC; 1.
SWART; SM00493; TOPIBC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C4-TYPE 1.
C4-TYPE 2.
C4-TYPE 3.
                                                                                                                                                                                                                                                                                             MEDLINE=20512582; PubMed=11058132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AP001515; BAB06186.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78910 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome.
                                    STANDARD;
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=C-125 / JCM 9153;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P06612; 1ECL
                                                                                                                                                                                                                   NCBI_TaxID=86665;
                                TOP1 BACHD 09KA23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FAMILY.
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ACT_SITE
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RESULT 51
TOP1_BACHD
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Gaps

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0; Indels

0; Mismatches

5; Conservative

Best Local Similarity

Matches

Query Match

100.0%; Score 23; DB 1; Length 602; 100.0%; Pred. No. 3.3e+02;

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693 EILDV 697
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                                                                                                                                                                                                                                            SEQUENCE
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BOVIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20193820; PubMed=10729156;
Afonso C.L., Tulman B.R., Lu Z., Zeak L., Kutish G.F., Rock D.L.;
"The genome of fowlpox virus.";
"The genome of fowlpox virus.";
-!- FUNCTION: ACTS WITH RNA POLYMERASE TO INITIATE TRANSCRIPTION FROM EARLY GENE PROMOTERS. A DNA-DEPENDENT ATPASE ACTIVITY IS
ASSOCIATED WITH VETF:
-!- SUBUNIT: HETERODIMER OF A 70 kDa AND A 82 kDa SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Sprague-Dawley; TISSUE=Brain; MEDLINE=9703143; Pubméd=8915891; Neuner-Jehle M., Denizot J.P., Borbely A.A., Mallet J.; Neuner-Jehle M., Denizot J.P., Borbely A.A., Mallet J.; Characterization and sleep deprivation-induced expression modulation of dendrin, a novel dendritic protein in rat brain neurons."; J. Neurosci. Res. 46:138-151(1996).
-i- MISCELLANEOUS: MODULATED BY SLEEP DEPRIVATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                  Fowlpox virus (FPV).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Early transcription factor 82 kDa subunit (VETF large subunit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 23; DB 1; Length 709; 100.0%; Pred. No. 4e+02; o. Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transcription regulation, Activator.
SEQUENCE 709 AA, 82729 MW; 79C39E93A84E051C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1997 (Rel. 35, Last annotation update)
Dendrin (Fragment)
                                                                                                                                                                              709 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             719 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100...
5; Conservative
                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10261;
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                                                              519 EILDV 523
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                  1 EILDV
                                                                                                                                                                           ETF2 FOWPV
Q9J562;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Cooperates with MD-2 and TLR6 to mediate the innate immune response to bacterial lipoproteins and other microbial cell wall components. Acts via MyD88 and TRR6, leading to NF-kappa-B activation, cytokine secretion and the inflammatory response. May also promote apoptosis in response to lipoproteins (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: Binds MD-2 and TLR6 via the extracellular domain. Binds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Guionaud C.T., Dubey C., Zumkehr J.R., Sonstegard T.S., Jungi T.W., "Role of bovine TLR2, TLR4 and CD14 in the recognition of bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butharia; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 23; DB 1; Length 719; 100.0%; Pred. No. 4e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Receptor; Immune response; Inflammatory response; Signal;
                                                                                                                                                                                                                                                                                                                                                                 719 AA; 77208 MW; 89E2ED094514EAFB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            095LA9; 09GL66;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Toll-like receptor 2 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   784 AA.
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InterPro; IPR000483; LRR Cterm.
InterPro; IPR000153; LRR Cterm.
Pfam; PP00560; LRR; 6.
Pfam; PP01463; LRRCT; 1.
Pfam; PP01582; TIR; 1.
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                                                                                                                                                                                                                                                                                               EMBL; X96589; CAA65407.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Conservative
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Best Local Similarity
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MEDLINE=98421677; PubMed=9751057;
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SIGNAL
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   060603; 015454;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Toll-like receptor 2 precursor (Toll/interleukin 1 receptor-like
                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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Drosophila
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Pred. No. 4.4e+02;
Leucine-rich repeat; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                             TOLL-LIKE RECEPTOR 2.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                       59FDB9DFA7984C18 CRC64;
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MEDLINE-98118556; PubMed-9435236;
Rock P.L., Hardiman G., Timans J.C., Kastelein R.A., Ra family of human receptors structurally related to Toll.";
                                                                     CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 95:588-593(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           784 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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MEDLINE=98261424; PubMed=9596645;
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                                                                                                                                                                                                                                                                                                                                                                                                       90204 MW;
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ilarity 100.0%;
Conservative 0
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  Repeat;
                114
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TLR2 OR TIL4.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                       442
784 AA;
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tes 5; Conserv
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 Transmembrane;
SIGNAL
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CARBOHYD
CARBOHYD
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DOMAIN
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REPEAT
REPEAT
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SEQUENCE
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response to bacterial lipoproteins and other microbial cell wall response to bacterial lipoproteins and other microbial cell wall components. Acts via MyD88 and TRAF6, leading to NF-Kappa-B activation, cytokine secretion and the inflammatory response. May also promote apoptosis in response to lipoproteins. Recognizes mycoplasmal macrophage-activating lipopeptide-kD (MALP-2), soluble tuberculosis factor (STF), phenol-soluble modulin (PSM) and B.burgdorferi outer surface protein A lipoprotein (OspA-L) cooperatively with TLR6.

-: SUBUNTT: Binds MD-2 and TLR6 via the extracellular domain. Binds MyD88 via their respective TIR domains.

-: SUBUNTT: Binds MD-2 and TLR6 via the extracellular domain. Binds LUCATION: Type I membrane protein (By similarity).

-: SUBCELLULAR LOCATION: Type I membrane protein lood and in spleen. Also detected in lung and in fetal liver. Levels are low in other tissues.

-: SIMILARITY: CONTAINS 10 THE TOLL-LIKE RECEPTOR FAMILY.

-: SIMILARITY: CONTAINS 11 TIR DOMAIN.

-: SIMILARITY: CONTAINS 11 TIR DOMAIN.
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Yang R.-B., Mark M.R., Gray A., Huang A., Xie M.H., Zhang M.,
Goddard A., Wood W.I., Gurney A.L., Godowski P.J.;
"Toll-like receptor-2 mediates lipopolysaccharide-induced cellular
                                                                                                                                                                                                                           RESPONSE TO BACTERIAL LIPOPROTEINS.
MIDLINE-99357867; PubMed-10426996.
Aliprantis A.O., Yang R.-B., Mark M.R., Suggett S., Devaux B.,
Radolf J.D., Klimpel G.R., Godowski P.J., Zychlinsky A.;
Cell activation and apoptosis by bacterial lipoproteins through
Toll-like receptor-2.
Science 285:736-739(1999).
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Leucine-rich repeat; Glycoprotein;
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TOLL-LIKE RECEPTOR 2.
EXTRACELLULAR (POTENTIAL)
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PDB: 1FYW; 22-NOV-00.
InterPro; 1PR001611; LRR.
InterPro; 1PR003591; LRR_Cterm.
InterPro; 1PR003591; LRR_typ.
InterPro; 1PR00151; TIR_domain.
Pfam; PP00560; LRR; 6...
Pfam; PP01463; LRR; f...
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SMART; SM00082; LRRCT; 1.
SMART; SM00369; LRR_TYP; 2.
SMART; SW00255; TIR; 1.
PROSITE; PS50104; TIR; 1.
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Transmembrane; Repeat; Leud
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor domains.";
Nature 408:111-115(2000).
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Nature 395:284-288(1998).
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EMBL; AB020807; BAA78631.1; -.
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Conservative (
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Genew; HGNC:16711; TLR6.
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SIGNAL 1
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es 5; Conserv
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
P->F ABOLISHES THE INTERACTION WITH
MYD88. NO EFFECT ON OLIGOMERIZATION ON THE STRUCTURE OF THE TIR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bulut Y., Faure E., Thomas L., Equils O., Arditi M., "Cooperation of Toll-like receptor 2 and 6 for cellular activation 1 soluble tuberculosis factor and Borrelia burgdorferi outer surface protein A lipoprotein: role of Toll-interacting protein and IL-1 receptor signaling molecules in Toll-like receptor 2 signaling "; J. Immunol. 167:987-994(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Participates in the innate immune response to Grampositive bacteria and fungi. Acts via MyD88 and TRAF6, leading to NF-kappa-B activation, cytokine secretion and the inflammatory response. Recognizes mycoplasmal macrophage-activating lipopeptide-2kD (MALP-2), soluble tuberculosis factor (STF), phenol-soluble modulin (FSM) and B.burgdorferi outer surface protein A lipoprotein (OSPA-L) cooperatively with TLR2. SUBUNIT: Binds TLR2 via their respective extracellular domains.
                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUB-Placenta;
MEDLINE=99250250; PubMed=10231569;
MEDLINE=99250250; PubMed=10231569;
Jakeuchi O., Kawai T., Sanjo H., Copeland N.G., Gilbert D.J.,
Jenkins N.A., Takeda K., Akira S.;
"TLRE: A novel member of an expanding Toll-like receptor family.";
Gene 231:59-65(1999).
                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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7DBE6B24CF1FAF8B CRC64;
CYTOPLASMIC (POTENTIAL)
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[5-JUN-2002 (Rel. 41, Last sequence update)
[5-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                            796 AA
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                        Foll-like receptor 6 precursor
                                                                                                                                                                                                 89837 MW;
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                            STANDARD;
sapiens (Human)
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784 AA;
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ID TLR6_HUMAN
AC Q9Y2C9;
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MUTAGEN
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Binds MyD88 via their respective TIR domains (By similarity).

-!- SUBCELLULAR LOCATION: Type I membrane protein. Plasma membrane and phagosomes (By similarity).

-!- TISSUE SPECIFICITY: Detected in monocytes, CD11c+ immature dendritic cells, plasmacytoid pre-dendritic cells and dermal microvessel endothelial cells.
-!- SIMILARITY: BELONGS TO THE TOLL-LIKE RECEPTOR FAMILY.
-!- SIMILARITY: CONTAINS 1 TIR DOMAIN.
-!- SIMILARITY: CONTAINS 13 LEUCINE-RICH REPEATS (LRR).
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
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InterPro; IPR000483; LRR_Cterm.
InterPro; IPR000483; LRR_Cterm.
InterPro; IPR000159; LRR_out.
InterPro; IPR000159; IRR_domain.
Pfam; PF01463; LRRCT; 1.
Pfam; PF01463; LRRCT; 1.
Pfam; PF01463; LRRCT; 1.
PRINTS; PR00019; LEURICHPPT.
SMART; SM000370; LRR; 2.
SMART; SM000255; TIR; 1.
PROSITE; PS50104; TIR; 1.
PROSITE; PS50104; TIR; 1.
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881 AA.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  spirochete.";
Science 281:375-388(1998).
-!- FUNCTION: DEGRADES SHORT-LIVED REGULATORY AND ABNORMAL PROTEINS IN
PRESENCE OF ATP. HYDROLYZES TWO ATPS FOR EACH PEPTIDE BOND CLEAVED
IN THE PROTEINS UBSTRATE (BY SIMILIARITY).
-!- CATALYTIC ACTIVITY: HYDROLYSIS Of large proteins such as globin,
casein and denaturated serum albumin, in presence of ATP.
-!- SUBDINT: HONOTERTAMER (BY SYMILIARITY).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: BELONGS TO PEPTIDASE PAMILY $16.
                                                                                                                                                                                                                                                                                                                                  STRAIN-Nichols,
MEDLINE=98332770; PubMed=9665876;
Fraser C.M., White O., Sutton G.G.,
Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.
Venter B., Hørst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                         Treponema pallidum.
Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
                                                                              30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ATF-dependent protease La (EC 3.4.21.53).
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                                                       30-MAY-2000 (Rel. 39, Created)
  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              HISSUE 98330437; PubMed=9664034; Marks P.W., Arai M., Bandura J.L., Kwiatkowski D.J.; Marks P.W., Arai M., Bandura J.L., Kwiatkowski D.J.; Marks P.W., Arai M., Bandura J.L., Kwiatkowski D.J.; Advillin (1992): a new member of the gelsolin/villin family of actin regulatory proteins...;
J. Call Sci. 111:2129-2136(1998).
J. Call Sci. 111:2129-2136(1998).
J. Call Sci. 111:2129-2136(1998).
J. Call Sci. 111:2129-2136(1998).
J. Call Sci. 111:2129-2136(1998).
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J. Call Sci. 111:2129-2136(1998).
J. Call Sci. 111:2129-2136(1998).
J. Call Sci. 111:2139(1998).

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                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         n-binding; Capping protein; Repeat.
CORE (BY SIMILARITY).
HEADPIECE (BY SIMILARITY).
GELSOLIN-LIKE' 1.
GELSOLIN-LIKE' 2.
GELSOLIN-LIKE' 3.
GELSOLIN-LIKE' 4.
GELSOLIN-LIKE 5.
GELSOLIN-LIKE 5.
VHP.
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SIMILARITY).
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                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                    819 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HISSP, P02640; 1VII.
InterPro; IPR001974; Gelsolin.
InterPro; IPR001974; Gelsolin.
Pfam; PF00205; Gelsolin; 6.
Pfam; PF02209; VHP; 1.
PRINTS; PR00597; GELSOLIN.
SMART; SM00262; GEL; 6.
SMART; SM00183; VHP; 1.
Cytoskeleton; Calcium; Actin-bin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF041449; AAC25051.1; -.
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                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Uterus;
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                                                                                 ADVL HUMAN
075366;
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REPEAT
REPEAT
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REPEAT
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InterPro; IPR003955,
InterPro; IPR001270; Chaprnin_c+F-.

R InterPro; IPR001270; Chaprnin_c+F-.

R InterPro; IPR001211; LON.

DR InterPro; IPR001984; Lon_endopep.

InterPro; IPR001984; Lon_fam.

DR Pfam; PF00004; AAA; 1.

DR PRINTS; PR00380; CLPPROTASEA.

DR SWART; SW00380; CLPPROTASEA.

DR SWART; SW00464; LON; 1.

DR SWART; SW00464; LON; 1.

DR Hydrolase; Serine profease; ATP-binding; Complete proteome.

WP PROSITE; PS01046; LON SER; 1.

DR Hydrolase; Serine profease; ATP-binding; Complete proteome.

WP BIND 440 447 ATP (POTENTIAL).

"DR Hydrolase; Serine profease; ATP-binding; Complete proteome.

"TAT 767 RS SMILARITY.

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llarity 100.0%; Pred. No. 5e+02;
Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDINIERS PROJECTOR PubMed=1946430;
A REDINIERS PROJECTOR PUBMed=1946430;
A REPLAIN S., Downey W.E., Tang C.K., Philpott C., Haile D.J.,
A Orloff D.G., Harford J.B., Rouault T.A., Klausner R.D.;
T. "A regulated RNA binding protein also possesses aconitase activity.";
Proc. Natl. Acad. Sci. U.S.A. 88:10109-10113(1991).
-!- FUNCTION: BINDS TO IRON-RESPONSIVE ELEMENTS (IRES), WHICH ARE STEM-LOOP STRUCTURES FOUND IN THE 5'TUR OF PERRATIN. AND DELTA ANINOLEVULINIC ACID SYNTHASE MRNAS, AND IN THE 3'UTR OF TRANSFERRIN RECEPTOR MRNA. BINDING TO THE 18'TUR OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE PROJECT OF THE 
                   "Expression of active iron regulatory factor from a full-length human cDNA by in vitro transcription/translation."; Nucleic Acids Res. 20:33-39(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rouault T.A., Tang C.K., Kaptain S., Burgess W.H., Haile D.J., Samaniego F., McBride O.W., Harford J.B., Klausner R.D.; "Cloning of the cDNA encoding an RNA regulatory protein -- the human
                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleogtomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=92150156; PubMed=1738601;
Hirling H., Emery-Goodman A., Thompson N., Neupert B., Seiser C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: CYtoplasmic.
SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hentze M.W., Argos P.;
"Homology between IRE-BP, a regulatory RNA-binding protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 53-889 FROM N.A., AND PARTIAL SEQUENCE MEDLINE=91045916; PubMed=2172968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          iron-responsive element-binding protein.";
Proc. Natl. Acad. Sci. U.S.A. 87:7958-7962(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY TO ACONITASES AND IPM ISOMERASES.
MEDLINE=91232935; PubMed=1903202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aconitase, and isopropylmalate isomerase.";
Nucleic Acids Res. 19:1739-1740(1991).
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EMBL; BC018103; AAH18103.1; -
EMBL; M58510; AAA69900.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACONITASE ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FISSUE=Uterus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kuehn L.;
                      IRE1_HUMAN
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-!- FUNCTION: THIS PROTEIN MATURES SS RRNA FROM ITS PRECURSORS FROM ALL THE RRNA GENES. IT IS THE MAJOR ENDORIBONUCLEASE PARTICIPATING IN MENA TURNOVER BY SIMILARITY.
-!- SUBUNIT: ORGANIZED INTO A STRUCTURE (PROCESSOME OR RNA DEGRADOSOME) CONTAINING A NUMBER OF RNA-PROCESSING ENZYMES (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                            FLVKKQDIENILHWNVTQH -> CPRKTRTQNLPPMLSNKL Y (IN REF. 3).
EIAO5AF701D46DCB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
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STRAIN=TOkyo 1998;
MEDLINE=20445173; PubMed=10993077;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
"Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. APS.";
                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY)
SIMILARITY)
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                                              InterPro; IEI.

InterPro; IEI.

Rem; PF00130; accnitase; 1.

Rem; PR00415; Aconitase; 1.

Rem; PR00415; Aconitase.

Rem; PR00511; Aconitase.

Resoirs; PS00456; Aconitase.

Resoirs; PS001244; Aconitase.

Resoirs; PS001244; Aconitase.

Remosirs; PS001244; 
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-- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
--- SIMILARITY: BELONGS TO THE RNE FAMILY.
--- SIMILARITY: CONTAINS 1 S1 MOTIF DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                symbiotic bacterium).
Bacteria; Proteobacteria; gamma subdivision; Buchnera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ribonuclease E (EC 3.1.4.-) (RNase E).
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SMART; SM00316; S1; 1.
TIGRFAMS; TIGR00757; RNaseEG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     889 AA; 98398 MW;
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InterPro; IPR004659; RNaseEG.
InterPro; IPR003029; S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.08;
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Genew; HGNC:117; ACO1.
MIM; 100880; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=118099;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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RNE_BUCAI
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Mismatches

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Conservative
                                      152 EİLDV 156
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                                                                                                                                                                                                                                                                                                                            Venter J.C.;
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                                                                  RESULT 62
HEPA_HAEIN
ID HEPA_HAEIN
   'n
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                     1 EILDV
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SITE
                                                                                                 P44781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
  Matches
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                                                                    ö
                                                                     Gaps
                                                                                                                                                                                                                                                                                                      PROSITE; PS50126; S1; 1.

PHOSITE; PS50126; S1; 1.

PHOTOLASE; Nuclease; Endonuclease; RNA-binding; Complete proteome. 3 DOMAIN
SEQUENCE 902 Aa; 104006 MW; C3FA00476E3C2E37 CRC64;
                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                    ö
                                                / Match 100.0%; Score 23; DB 1; Length 902; Local Similarity 100.0%; Pred. No. 5.1e+02; Nes 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 23; DB 1; Length 919; 100.0%; Pred. No. 5.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PSS0297; ANK REPEAT; 1.
PROSITE; PSS0297; ANK REP REGION; 1.
Colled Coil; Repeat; NK Fepeat.
REPEAT 384 413 ANK 1.
REPEAT 419 448 ANK 1.
REPEAT 455 485 ANK 4.
DOMAIN 515 552 COILED COIL (POTENTIAL).
REPEAT 603 632 ANK 5. FOOTENTIAL).
REPEAT 699 729 ANK 6. (POTENTIAL).
SEQUENCE 919 AA; 100380 MW; SCB0022B0024EEA4 CRC64;
                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update).
16-OCT-2001 (Rel. 40, Last annotation update)
Symphilin 1 (Alpha-symuclein interacting protein).
                                                                                                                                                          919 AA
                                                                                                                                                                                                                                                                                     TISSUE=Brain;
MEDLINE=99251592; PubMed=10319874;
                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF076929; AAD30362.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HGNC:11139; SNCAIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIM; 603779; -.
InterPro; IPR002110; ANK.
Pfam; PF00023; ank; 4.
SMART; SM00248; ANK; 2.
                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                              SEQUENCE PROM N.A.
                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                         525 KILDV 529
                                                                                       1 BILDV 5
                                                                                                                                                          SYNP HUMAN
                                                 Query Match
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Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAINSER / KW20 / KW20 / ATCC 51907;
MEDLINE=55350630; PubMed=7542800;
MEDLINE=55350630; PubMed=7542800;
Pleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Karlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutron G., Fitzhugh W., Fields C.A., Gocayne J.D., Mcidman J.F., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Ghin L.D., Pritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                            01-NOV-1995 (Rel. 32, Created)
1-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
RNA polymerase associated protein homolog (ATP-dependent helicase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 269:496-512(1995).
-!- SUBUNIT: BINDS TO THE RNA POLYMERASE (RNAP) (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE SNP2/RAD54 HELICASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 23; DB 1; Length 923; 100.0%; Pred. No. 5.3e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8022403581DAADBD CRC64;
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923 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               949 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SMO0490; HELICC; 1.
SMART; SMO0490; HELICC; 1.
Helicase; ATP-binding; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEAH BOX
PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001650; Helicase_C.
InterPro; IPR000330; SNP2_N.
Pfam; PP00176; SNP2_N; 1.
Pfam; PP00271; helicase_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104405 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U32744; AAC22275.1; -.
TIGR; H10616; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
STANDARD;
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                                                                                                                                                                                                                                                           Haemophilus influenzae.
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les 5, Conserv
                                                                                                                                                                                                                                                                                                                                                        NCBI TaxID=727;
                                                                                                                                                                                                                         HEPA OR HI0616.
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ID GLND_RHIME
AC P56884;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAINSCY. Columbia;

MEDLINE-20083488; PubMed=10617198;

MEDLINE-20083488; PubMed=10617198;

MAPER K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,

MARYER E., Ansorge W., Brandt P., Grivell L.A., Rieger M.,

Meichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,

Meichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,

Kreis M., Delseny M., Juddomench P., Watson M., Schmidtheini T.,

Meichert B., Portetelle D., Perez-Alonso M., Bancroft I.,

Nos P., Hoheisel J., Zimmermann M., Wedler H., Ridley P.,

Langham S.-A., McCullagh B., Bliham L., Robben J.,

Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,

Meitzenegger T., Bothe G., Rampsperger U., Hilbert H., Braun M.,

Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,

Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,

Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,

Meneiser S., Hempel S., Feldgausch M., Lamberth S., Van den Daele H.,

Merksen S., Hempel S., Feldgausch M., Lamberth S., Van den Daele H.,

Merksen S., Hempel S., Feldgausch M., Lamberth S., Van den Daele H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Preprotein translocase seck subunit, chloroplast precursor.
SECA OR AT4G01800 OR T7B11.6.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                             Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 23; DB 1; Length 952; 100.0%; Pred. No. 5.4e+02; tive 0; Mismatches 0; Indels
  Hypothetical 105.3 kDa protein C01G6.5 in chromosome III
                                                                                                                                                                                                                                                             Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39 100 FHA.
952 AA; 105274 MW; D9CFB0AB3C685FBE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, 235595, CAA84636.1; -.. WormPep, C01G6.5; CE00867.
InterPro; IPR000253; FHA_domain.
Pfam, PF00498; FHA; 1..
PROSITE; PS50006; FHA, 1..
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.0%;
ses 5; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                     Caenorhabditis elegans.
                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI TaxID=3702;
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Q9SYIO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                        Berks M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 65
SECA_ARATH
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Matches
          셤
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Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
Renard C., Thabault P., Vandenhol M., Waidner S., Galibert F.;
Analyais of the chromosome sequence of the legume symbiont
Froc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
---FUNCTION: MODIFIES, BY URIDYLYLATION OR DEURIDYLYLATION THE PII
(GLNB) REGULATORY PROTEIN (BY SIMILARITY).
----CATALYIC ACTIVITY: UTP + [protein-FII] = diphosphate + uridylyl-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=21172888; PubMed=11274131;
Rudnick P.A., Arcondeguy T., Kennedy C.K., Kahn D.;
"glnD and mviN are genes of an essential operon in Sinorhizobium
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-UDN-2002 (Rel. 41, Last annotation update)
15-UDN-2002 (Rel. 41, Last annotation update)
[Protein-PII] uridylyltransferase (EC 2.7.59) (PII uridylyl-
transferase) (Uridylyl removing enzyme) (UTase).
GLND OR R00396 OR SWC01124.
Rhizobium meliloti (Sinorhizobium meliloti).
Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transferase; Nucleotidyltransferase; Nitrogen fixation; Complete proteome. SEQUENCE 949 AA; 106381 MW; BF549C1R0DR540A0 PPCA4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO THE GLND FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002819; HD.
InterPro; IPR003607; ME Pplase HDC.
InterPro; IPR002934; NTP_transf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteriol. 183:2682-2685(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF01842; ACT; 2.
Pfam; PF01909; NTP_transf_2; 1.
Pfam; PF01966; HD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF227730; AAF37852.1; -. EMBL; AL591783; CAC41833.1; -. InterPro; IPR002912; ACT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00471; HDC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [protein-PII]
                                                                                                                                                                                                                                     NCBI_TaxID=382;
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01-NOV-1995
01-NOV-1995
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P46012; RESULT 64 YKIS_CAEEL ID YKIS_C. AC P46012 DT 01-NOV DT 01-NOV

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Gaps

MEDLINE=99000842; PubMed=9782088; Xia C., Rahman A., Yang Z., Goldstein L.S.B.; "Chromosomal localization reveals three kinesin heavy chain genes in

SEQUENCE FROM N.A. NCBI_TaxID=10090;

TISSUE=Brain;

mouse.

J. Cell Biol. 119:1287-1296(1992).

Aizawa H., Sekine Y., Takemura R., Zhang Z., Nangaku M., Hirokawa N.; "Kinesin family in murine central nervous system.";

TISSUE=Brain; MEDLINE=93077686; PubMed=1447303; SEQUENCE OF 89-231 FROM N.A. Genomics 52:209-213(1998).

01-OCT-1993 (Rel. 27, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
Neuronal kinesin heavy chain (NKHC) (Kinesin heavy chain isoform 5A)
(Kinesin heavy chain neuron-specific 1).
KIRS ON KIRS ON KHRC1.
Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

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SOLITIFIE TO BE SEED TO SOLITION OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECO
Van Montagu M., Rogers J., Cronin A., Quail, M., Bray-Allen S.,
Retett L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
Rettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
Borkova D., Bloecker H., Scharfe M., Benes V., Rechmann S.,
Borkova D., Bloecker H., Scharfe M., Granderath K., Loehnert T.-H.
Agbel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A.,
Ra Gebel C., Fuchs W., Fartmann B., Granderath K., Paluer D., Herzl A.,
Ra Neumann S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
Rochabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
R. Schmabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
R. Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
R. Schmabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
R. Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
R. Heijnen L., Schwarz S., Scholler P., Heber S., Francs P., Bielke C.,
R. Frishman D., Hasse D., Lemcke K., Mewes H.-W., Stocker S.,
R. Zeccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
R. Accaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
R. Accaria P., Bentley D., Sheet P., Cordes M., Abu-Threideh J.,
Schneil S., Scholler P., Cordes M., Abu-Threideh J.,
R. Kramer J., Fulton B., Miller N., Greco T., Kemp K.,
Kramer J., Fulton B., Mardis E., Dante M., Pepin K., Hiller L.,
R. Kramer J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
R. Attonoùu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
R. Kramer S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
R. Kraner S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
R. Kraner S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
R. Kraner S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
R. Kraner S., Shohdy N., Martienssen R., Miller M., Holdin J., Till S.,
R. Kaner S., Shohdy N., Martienssen R., Miller M., Holdin J., Thill S.,
R. Kaner M., Martienssen R., Miller M., Holdin R., Marta M., Martienssen R., Marta M., Marta M., Marta M., Marta M., Marta M., M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein transport, ATP-binding, Chloroplast, Translocation, Transport, Transit peptide. 1 ? CHLOBODIACT (ACCUMUNITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: CHLOROPLAST STROMA. A MINOR FRACTION IS ASSOCIATED WITH THE THYLAKOID MEMBRANE. SIMILARITY: BELONGS TO THE SECA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHLOROPLAST (POTENTIAL).
PREPROTEIN TRANSLOCASE SECA SUBUNIT.
ATP (POTENTIAL).
WW; 3D2AE013DB347187 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 402:769-777(1999).
-!- FUNCTION: INVOLVED IN PROTEIN EXPORT. LIKELY PARTICIPATES IN PROTEIN TRANSLOCATION ACROSS THE THYLAKOID MEMBRANE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 23; DB 1; Length 1021; 100.0%; Pred. No. 5.9e+02;
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1021 AA; 115114 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interpro; IPR000185; SecA.
Pfam; PF01043; SecA protein; 1.
PRINTS; PR00906; SECA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AC007138; AAD22642.1; -. EMBL; AL161492; CAB77750.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGRFAMS; TIGR00963; SECA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE, PS01312, SECA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183
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SEQUENCE
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PROTEIN THAT MAY PLAY A ROLE IN ORGANELLE TRANSPORT.

-- SUBUNIT: OLIGOMER COMPOSED OF TWO HEAVY CHAINS AND TWO LIGHT CHAINS (BY STMILARITY).

-- SUBCELLULAR LOCATION: CONCENTRATED IN THE CELL BODY OF THE NEURONS, PARTICULARLY IN THE PERINUCLEAR REGION.

-- DOMAIN: COMPOSED OF THREE STRUCTURAL DOWAINS: A LARGE GLOBULAR N-TERMINAL DOMAIN WHICH IS RESPONSIBLE FOR THE MOTOR ACTIVITY OF KINESIN (IT HYDROLYZES APP AND BINDS MICROTUBLIE), A CENTRAL ALPHA-HELICAL COILED COIL DOMAIN THAT MEDIATES THE HEAVY CHAIN DIMERIZATION; AND A SMALL GLOBULAR C-TERMINAL DOMAIN WHICH INTERACTS WITH OTHER PROTEINS (SUCH AS THE KINESIN LIGHT CHAINS), VESICLES AND MEMBERANGO SRGANELLES.

-- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. KINESIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Сарв
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PIR; C44259; C44259.

R HSSP; P56536; ZkIN.

JR MGD; MGI:109564; Kif5a.

DR InterPro; PR001752; Kinesin_motor.

DR PRONIE; P800429; KINESINHEAVY.

DR PROSITE; P800419; KINESINHEAVY.

DR PROSITE; P800419; KINESINHEAVY.

DR PROSITE; P850067; KINESIN MOTOR DOMAIN1; 1.

DR PROSITE; P850067; KINESIN MOTOR DOMAIN2; 1.

RW MOTOR protein; Microtubules; ATP-binding; Coiled coil.

KW MOTOR protein; Microtubules; ATP-binding; Coiled coil.

FT DOMAIN 331 906 COILED COILED

TOMAIN 331 906 COILED COILE

TOMAIN 315 MICROTUBULE.BINDING.

174 315 MICROTUBULE.BINDING.

174 315 MICROTUBULE.BINDING.

175 A48D2FD794B9194 CRC64;

L-> P (NN REF. 2).

244B2FD794B9194 CRC64;
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; Pred. No. 5.9e+02;
0; Mismatches 0;
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Best Local Similarity
Matches 5, Conserv
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Gapa

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0; Mismatches

Local Similarity 100. nes 5; Conservative

Matches

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PRT; 1027 AA.

STANDARD;

KINN MOUSE ID KINN MOUSE S AC P33175; Q922F9;

RESULT 66

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Gaps

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Mismatches

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                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: CONCENTRATED IN THE CELL BODY OF THE NEURONS, PARTICULARLY IN THE PERINUCLEAR REGION.

TISSUE SPECIFICITY: DISTRIBUTED THROUGHOUT THE CNS BUT IS HIGHLY ERRICHED IN SUBSETS OF NEURONS.

DOWAIN: COMPOSED OF THREE STRUCTURAL DOMAINS: A LARGE GLOBULAR N-TERMINAL DOMAIN WHICH IS RESPONSIBLE FOR THE MOTOR ACTIVITY OF KINESIN (IT HYDROLYZES ATP AND BINDS MICROTUBLE), A CENTRAL ALPHA-HELICAL COLLED COIL DOMAIN THAT MEDIATES THE HEAVY CHAIN DIMERIZATION; AND A SMALL GLOBULAR C-TERMINAL DOMAIN WHICH INTERACTE WITH OTHER PROTEINS (SUCH AS THE KINESIN LIGHT CHAINS),
                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2010 (Rel. 40, Last annotation update)
Neuronal kinesin heavy chain (NKHC) (Kinesin heavy chain isoform 5A)
(Kinesin heavy chain neuron-specific 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. KINESIN SUBFAMILY.
                                                                                                                                                                                                                                                                        TISSUE-Hippocampus;

BEDLINE-2442426; Pubmed-7514426;

Niclas J., Navnon F., Hom-Booher N., Vale R.D.;

"Cloning and localization of a conventional kinesin motor expressed
                                                                                                                                                                                                                                                                                                                                    Neuron 12:1059-1072(1994).
-!- FUNCTION: KINESIN IS A MICROTUBULE-ASSOCIATED FORCE-PRODUCING
--- PROTEIN THAT MAY PLAY A ROLE IN ORGANELLE TRANSPORT.
-!- SUBUNIT: OLLGOMER COMPOSED OF TWO HEAVY CHAINS AND TWO LIGHT
                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; FROUSS; ISC, 1.

RMO129; KISC, 1.

PROSITE; PSO067; KINESIN_MOTOR_DOMAIN1; 1.

PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.

MOTOR_DROTEIN; Microtubules; ATF-binding; Coiled coil.

KINESIN_MOTOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MICROTUBULE-BINDING.
ATP (BY SIMILARITY).
W; 04C0C12342020794 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VESICLES AND MEMBRANOUS ORGANELLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLOBULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIM, 602821, -...
InterPro, IPR001752, kinesin_motor.
Pfam, PP00225, kinesin, 1.
PRINTS, PR00380, KINESINHEAVY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genew; HGNC:6323; KIF5A.
                                                                                                                                                                                                                                                                                                                        exclusively in neurons.
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315
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86 9
1032 AA;
                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                        179 EILDV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P56536;
 ß
EILDV
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NP BIND
SEQUENCE
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Length 1032;

Score 23; DB 1; Pred. No. 5.9e+02;

100.0%;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=015:H7 / RIMD 0509952;
MEDLINB=21156211; PubMed=11258796;
MEDLINB=21156211; PubMed=11258796;
MEDLINB=21156211; PubMed=11258796;
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.,
"Complete genome sequence of enterchemorrhagic Escherichia coli
"Complete genome sequence of enterchemorrhagic Escherichia coli
0157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=015:H7 / EDL933 / ATCC 700927;

MEDLINE=21074935; PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.,

"Genome sequence of enterchaemorrhagic Escherichia coli O157:H7.";
                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria, Proteobacteria, gamma subdivision, Enterobacteriaceae,
Bscherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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938 938 IRON-SULFUR (4FE-4S) (POTENTIAL)
941 IRON-SULFUR (4FE-4S) (POTENTIAL)
944 944 IRON-SULFUR (4FE-4S) (POTENTIAL)
948 948 IRON-SULFUR (4FE-4S) (POTENTIAL)
948 115563 MW; C032E7D2956E738C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1032;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 23; DB 1; I
Pred. No. 5.9e+02;
                                                                                                                                                                                                                                                                     (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                             PRT; 1032 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE005518; AAG58007.1; -.
EMBL; AP002563; BAB37174.1; -.
InterPro; IPR001450; 4Fe4S ferredoxin.
InterPro; IPR001327; FAD pyr redox.
InterPro; IPR000205; NAD binding.
Pfam; PF00037; fer4; 1.
Pfam; PF00070; pyr redox; 1.
PRIMT; PF00070; pyr redox; 1.
PRIMT; PF00198; 4FE4S FERREDOXIN; 1.
Hypothetical protein; Iron-sulfur; 4Fe-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
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                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein ygfk.
YGFK OR Z4217 OR ECS3751.
Escherichia coli 0157:H7.
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                                                                                                                                                                                                             STANDARD;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=83334;
                                                           179 EILDV 183
ß
                                                                                                                   YGFK ECOS7

YGFK ECOS7

ID YGFK ECOS7

AC Q8XD75;
                                                                                                                                                                                                                                                                     15-JUN-2002
15-JUN-2002
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1 EILDV
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Spermatophyta; Magnoliophyta; eudicotyledona; core eudicots;
Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
NCBI_TaxID=3562;
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Matches 5; Conservative
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1036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       357 BILDV 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EILDV 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ULS7 OR DBP.
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SEQUENCE
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                                                                                                                                                                                                                                     spinach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 71
DNBI MCMVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                     SECUENCE FROM N.A.
STRAIDSIZ J. MG1625.
STRAIDSIZ J. MG1627; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perma N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spinacia oleracea (Spinach).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                Bacteria, Proteobacteria, gamma subdivision, Enterobacteriaceae,
Escherichia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 protein; Iron-sulfur; 4Fe-4S; Complete proteome.
938 938 IRON-SULFUR (4FE-4S) (POTENTIAL)
941 1RON-SULFUR (4FE-4S) (POTENTIAL)
944 944 IRON-SULFUR (4FE-4S) (POTENTIAL)
948 1894 IRON-SULFUR (4FE-4S) (POTENTIAL)
948 115581 MW; 588055851BE89648 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 23; DB 1; Length 1032; 100.0%; Pred. No. 5.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Preprotein translocase secA subunit, chloroplast precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                  046811;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypochetical protein ygfK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1036 AA
                                                                                                                                     PRT; 1032 AA
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InterPro; IPR001450; 4Fe4S ferredoxin.
InterPro; IPR001327; FAD pyr redox.
InterPro; IPR00205; NAD binding.
Pfam; PF00037; fer4; 1.
Pfam; PF000109; pyr redox; 1.
ProDom; PD0001199; FAD pyr redox; 1.
PROSITE; PS00198; 4FE4S_FERREDOXIN; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U28375; AAA83059.1; -.
EMBL; AE000371; AAC75916.1; -.
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Matches 5; Conservative
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                                                                                                                                     STANDARD;
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             267 EILDV 271
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Q36795;
                                                                                                                                     YGFK ECOLI
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                                                                                       RESULT 69
TO YGFK ECOLI
TO YGFK ECOLI
D TIS-JUN
DT 15-JUN
DE BRICH
CC BRCHET
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SECA_SPIOL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGREAMS; TIGRO0963; secA; 1.
PROSITE; PS01312; SECA; 1.
Protein transport; ATP-binding; Chloroplast; Translocation; Transport; Transit peptide.
1 776 CHLOROPLAGT (DOTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                          Berghoefer J., Karnauchov I., Herrmann R.G., Kloesgen R.B.; "Isolation and characterization of a cDNA encoding the SecA protein from spinach chloroplasts. Evidence for azide resistance of Sec-dependent protein translocation across thylakoid membranes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93033129; PubMed=1329325; Messerle M., Keil G.M., Schneider K., Koszinowski U.H.; Messerle M., Keil G.M., Schneider K., Koszinowski U.H.; Characterization of the murine cytomegalovirus genes encoding the major DNA binding profein and the ICP18.5 homolog."; Virology 191:355-367(1992).
-!- FUNCTION: SINGLE-STRAND DNA-BINDING PROTEIN REQUIRED FOR DNA REPLICATION.
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: CHLOROPLAST STROMA. A MINOR FRACTION IS ASSOCIATED WITH THE THYLAKOID MEMBRANE. -!- SIMILARITY: BELONGS TO THE SECA PAMILY.
                                                                                                                                                                                                                                                                                                              J. Biol. Chem. 270:18341-18346 (1995).
-!- FUNCTION: INVOLVED IN PROTEIN EXPORT. LIKELY PARTICIPATES IN PROTEIN TRANSLOCATION ACROSS THE THYLAKOID MEMBRANE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 CHLOROPLAST (POTENTIAL).

PREPROTEIT TRANSLOCASE SECA SUBUNIT.

93 ATP (POTENTIAL).

116608 MW; 23920878B49A3283 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murine cytomegalovirus (strain Smith).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Muromegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          230672;
01-ARR-1993 (Rel. 25, Created)
01-ARR-1993 (Rel. 25, Last sequence update)
01-CCT-2001 (Rel. 40, Last annotation update)
Major DNA-binding protein (MDBP).
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SEQUENCE FROM N.A.
STRAIN-cv. Monatol; TISSUE-Leaf;
MEDLINE-95355455; PubMed-7629156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro, IPR000185; SecA.
Pfam; PF01043; SecA_protein; 1.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             767 EILDV 771
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SEQUENCE
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MEDLINE=21156231; PubMed=11258796;
Hayabhi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- PTM: Activation requires a sequential transfer of a phosphate group from a His in the primary transmitter domain, to a Asp in the receiver domain and to a His in the secondary transmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
Nature 409:529-533(2001).
SIMILARITY: BELONGS TO THE HERPESVIRUSES DNA-BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-0157:H7 / EDL933 / ATCC 700927;

MEDLINE=21074935; PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Rosefai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Bscherichia.
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                                                                                                                                                                                                                                                        100.0%; Score 23; DB 1; Length 1191; 100.0%; Pred. No. 6.9e+02;
                                                                                                                                                                          Pfam; PF00747; virai DNA_bp; 1.
DNA-binding; DNA replication; Zinc-finger; Nuclear protein;
                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                             1191 AA; 131640 MW; SBA4A7F07D7E1B9A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Engor protein evgS precursor (EC 2.7.3.-).
EVGS OR Z3632 OR ECS3249.
                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1197 AA
                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                    C2HC-TYPE
                                                                                                                                     EMBL, X67021, CAA47414.1, -.
PIR, A44051, A44051.
InterProj IPR000635, Viral_DNA_bind.
                                                                                                                                                                                                                                           Query Match
Best Local Similarity 10v...
".hes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli O157:H7
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ZN FING 47
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PHOSPHORYLATION (BY SIMILARITY).
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Escherichia
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domain (By similarity).
-!- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
-!- SIMILARITY: CONTAINS 1 RESPONSE REGULATORY DOMAIN.
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CYTOPLASMIC (POTENTIAL).
POTENTIAL.
PERIPLASMIC (POTENTIAL).
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RESPONSE REGULATORY.
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                                                                                                                                                                                                                                                                                                                                                              EMBL, AB002561; BAB36672.1; ...
InterPro; IPR0043594; ATPbind ATPase.
InterPro; IPR0043594; HIS KIN sig.
InterPro; IPR004359; HIS KIN sig.
InterPro; IPR004361; High kinā.
InterPro; IPR001361; Hpt.
InterPro; IPR001311; SBP/glu_receptor.
InterPro; IPR001311; SBP/glu_receptor.
InterPro; IPR001313; SBP_bac_3.
InterPro; IPR001538; SBP_bac_3.
InterPro; IPR001538; SBP_bac_3.
InterPro; IPR001538; HarPase c; 1.
SWART; SW00073; HPT; 1.
SWART; SW00062; PBPD; 2.
SWART; SW0062; PBPD; 2.
SWART; SW0062; PBPD; 2.
SWART; SW0064; HEKA; 1.
PROSITE; PS50109; HIS KIN; 1.
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or send an email to license@isb-sib.ch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97349980; PubMed=9205837; MEDLINE=97349980; PubMed=9205837; MEDLINE=97349980; PubMed=9205837; MEDLINE=97349980; PubMed=9205837; Makine Y., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N., Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H., Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Uehara K., Wada C., Yamagata S., Horiutoh T., Meda J., Horiutoh T., Ronstruction of a contiguous 874-kb sequence of the Escherichia coli "Ki sequence features."; Makin on the linkage map and analysis of its sequence features.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-98134702; PubMed=9535079;
Perraud A.-L., Kimmel B., Weiss V., Gross R.;
Perraud A.-L., Kimmel B., Weiss V., Gross R.;
Fyedificity of the Bryak and Bryaks phosphorelay is mediated by the C-terminal HPt domains of the sensor proteins.";
Mol. Microbiol. 27:815-887 (1998).
-I- FUNCTION: Member of the two-component regulatory system evgs/evgA.
Phosphorylates evgA via a four-step phosphorelay in response to
                                                                                                                                                                                                                   Utsumi R., Katayama S., Ikeda M., Igaki S., Nakagawa H., Miwa A., Taniguchi M., Noda M.;
"Cloning and sequence analysis of the evgAS genes involved in signal transduction of Escherichia coli K-12.";
Nucleic Acids Symp. Ser. 27:149-150(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Probable).

PTM: Activation requires a sequential transfer of a phosphate group from a His in the primary transmitter domain, to a Asp in the receiver domain and to a His in the secondary transmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           environmental signals.
SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                          Kato A., Ohnishi H., Yamamoto K., Furuta E., Tanabe H., Utsumi R.; "Transcription of emrKY is regulated by the EvgA-EvgS two-component system in Escherichia coli K-12."; Biost. Biotechnol. Biochem. 64:1203-1209(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
STRAIN=K12;

MEDLLNES94171083; PubMed=8125343;

Utsumi R., Katayama S., Taniguchi M., Horie T., Ikeda M., Igaki :
Nakagawa H., Miwa A., Tanabe H., Noda M.;

"Newly identifiaed genes involved in the signal transduction of
Escherichia coli K-12.";

Gene 140:73-77(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997)
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                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (VARIANTS EVGS1 AND EVGS4).
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                                                                                                                                                                                                       WEDLINE=93173621; Pubmed=1289796;
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R SMARY; SM00387; HATPARSe_c; 1.

R SMARY; SM00037; HPT; 1.

SMART; SM000073; HPT; 1.

R SMART; SM00062; PBD; 2.

R R SMART; SM000448; REC; 1.

R PROSITE; PS50110; RESPONSE_REGULATORY; 1.

R PROSITE; PS50110; RESPONSE_REGULATORY; 1.

R PROSITE; PS50110; RESPONSE_REGULATORY; 1.

R PROSITE; PS50110; RESPONSE_REGULATORY; 1.

R PROSITE; PS50110; RESPONSE_REGULATORY; 1.

R PROSITE; PS50110; RESPONSE_REGULATORY; 1.

R PROSITE; PS50110; RESPONSE_REGULATORY; 1.

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POTENTIAL.
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ID _RPOD_SYNY3 STANDARD; PRT; 1317 AA, AC P73374;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
Conservative
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completed: February 8, 2003, 10:24:03
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                                                                                               SEQUENCE FROM N.A.

MEDLINE=97061201; PubMed=8905231;

MEDLINE=97061201; PubMed=8905231;

Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,

Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,

Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,

Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,

Yamada M., Yasuda M., Tabata S.,

"Sequence analysis of the genome of the unicellular cyanobacterium

Synechocystis sp. strain PCC6803. II. Sequence determination of the
entire genome and assignment of potential protein-coding regions.";

DNA Res. 3:109-116(1996).

I- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UTN-2002 (Rel. 41, Last annotation update)
DNA polymerase II large subunit (EC 2.7.7.7) (Pol II) [Contains: Hsp-NRC1 polc intein (Hsp-NRC1 polz intein)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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MEDLINE=20504483; PubMed=11016950;
NG W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 100.0%; Score 23; DB 1; Length 1317; Local Similarity 100.0%; Pred. No. 7.7e+02; nes 5; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00623; RNA_pol_A; 1.-
Pfam; PF01854; RNA_pol_A2; 2.
Transferase; DNA-directed RNA polymerase; Transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1317 AA; 144776 MW; 27B6970469E7E551 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Archaea, Euryarchaeota, Halobacteria, Halobacteriales,
Halobacteriaceae, Halobacterium.
NCBI_TaxID=64091;
                                           Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chrococcales; Synechocystis.
16-OCT-2001 (Rel. 40, Last annotation update)
DNA-directed RNA polymerase delta chain (EC 2.7.7.6)
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SEQUENCE 1317 AA
                             RPOC2 OR SLL1789
                                                                   NCBI_TaxID=1148;
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DP2L HALN1
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.,
"Genome sequence of Halbacterium species NRC-I.",
Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181 (2000).
-!- FUNCTION: POSSESSES TWO ACTIVITIES: A DNA SYNTHESIS (POLYMERASE)
AND AN EXCONCLEDINITY THAT DEGRADES SINGLE STRANDED DNA
IN THE 3' TO 5' DIRECTION. HAS A TEMPLATE-PRIMER PREFERENCE WHICH
IS CHARACTERISITIC OF A REPLICATIVE DNA POLYMERASE (BY SIMILMAITY).
-!- CALLALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSP-NRC1 POLC INTEIN (POTENTIAL).
DNA POLYMERASE II LARGE SUBUNIT, 2ND PART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTM: THIS PROTEIN UNDERGOES A PROTEIN SELF SPLICING THAT INVOLVES A POST-TRANSLATIONAL EXCISION OF THE INTERVENING REGION (INTEIN) FOLLOWED BY PEPTIDE LIGATION (POTENTIAL). SIMILARITY: BELONGS TO THE ARCHAEAL DNA POLYMERASE II FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50818; INTEIN C TER; FALSE NEG.
PROSITE; PS50817; INTEIN N TER; 1.
Transferame; DNA-directed DNA polymerame; DNA replication; Hydrolame;
Nucleame; Exonucleame; DNA-binding; Multifunctional enzyme;
Autocatalytic cleavage; Protein splicing; Complete proteome.

CHAIN 1 925 DNA POLYMERASE II LARGE SUBUNIT, 1ST PAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SUBUNIT: HETERODIMER OF A LARGE SUBUNIT AND A SMALL SUBUNIT (BY SIMILARITY).
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1370 AA; 150295 MW; 07878AA9976790C9 CRC64;
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InterPro, IPR003586, Hedgehog_hintC.
InterPro, IPR003587, Hedgehog_hintN.
InterPro, IPR002203, Intein.
InterPro, IPR004475, PolC_DP2.
SMART, SM00305, HintC, 1.
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Matches 5; Conserv
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17 23 100.0 159 11 QBR1U7 159 12 100.0 164 17 QBRSVG3 19 23 100.0 164 17 QBRZZZZ 23 100.0 169 16 QBZZZZZ 23 100.0 177 16 QBZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZ	23 100.0 324 15 23 100.0 333 16 23 100.0 333 16 23 100.0 333 17 23 100.0 334 2 23 100.0 344 2 23 100.0 344 2 23 100.0 344 2 23 100.0 351 3 23 100.0 351 3 23 100.0 350 10 23 100.0 366 16 23 100.0 366 16 23 100.0 367 10 23 100.0 368 10 23 100.0 368 10 23 100.0 368 10 23 100.0 368 10 23 100.0 368 10 23 100.0 368 10 23 100.0 368 10
n 5.1.3 Compugen Ltd. ; Search time 28 Seconds (without alignments) 36.794 Million cell updates/sec duesmeters: 222meters: 222meteris: balance to have a core of the result being printed, all score distribution.	Description P82341 pisum sativ Q97134 pisum sativ Q97134 neurospora Q87412 clostridium Q87412 dostridium Q87412 mus musculu Q91481 mus musculu Q91481 rattus norv Q91480 rattus norv Q91480 rattus norv Q91480 rattus norv Q91480 sattus norv Q91812 zprococcus Q87913 sechaeoglob Q9499 halobacteri Q889135 escherichia Q887915 escherichia
GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen OM protein - protein search, using sw model Run on: Pebruary 8, 2003, 10:22:23 ; Search t Without al 36.794 Mill Title: US-09-251-073A-16 Perfect score: 23 Searched: 1 ELLDV 5 Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 671580 seqs, 206047115 residues Total number of hits satisfying chosen parameters: Minimum DB seq length: 200000000 Post-processing: Minimum Match 100* Maximum Match 100* Maximum Match 100* Database: SPTERMBL 21:* 1: sp_archea:* 2: sp_bacteria:* 3: sp_human:* 3: sp_human:* 4: sp_human:* 5: sp_human:* 5: sp_human:* 6: sp_hammin:* 10: sp_hame:* 11: sp_varchea:* 12: sp_hame:* 13: sp_vartebrate:* 14: sp_unclassified:* 15: sp_hatcheap:* 16: sp_hatcheap:* 17: sp_archeap:* 16: sp_hatcheap:* 17: sp_archeap:* 16: sp_hatcheap:* 16: sp_hatcheap:* 17: sp_archeap:* 16: sp_hatcheap:* 16: sp_hatcheap:* 17: sp_archeap:* 18: sp_vartebrate:* 18: sp_vartebrate:* 19: sp_hatcheap:* 10: sp_hatcheap:* 10: sp_hatcheap:* 11: sp_archeap:* 12: sp_hatcheap:* 13: sp_vartebrate:* 14: sp_archeap:* 15: sp_hatcheap:* 16: sp_hatcheap:* 17: sp_archeap:* 18: sp_vartebrate:* 18: sp_vartebrate:* 19: sp_hatcheap:* 10: sp_hatcheap:* 10: sp_hatcheap:* 11: sp_archeap:* 12: sp_archeap:* 13: sp_archeap:* 14: sp_archeap:* 15: sp_archeap:* 16: sp_hatcheap:* 17: sp_archeap:* 18: sp_archeap:* 18: sp_archeap:* 19: sp_archeap:* 10: sp_arche	Result Core Match Length DB ID 23 100.0 14 10 P82341 23 100.0 50 16 Q92719 3 23 100.0 50 16 Q92719 4 23 100.0 50 16 Q92719 5 23 100.0 91 2 Q8VMP3 6 23 100.0 110 11 Q9JKS1 7 23 100.0 117 11 Q9JKS1 8 23 100.0 117 11 Q9JKS1 9 23 100.0 117 11 Q9JKS1 11 23 100.0 119 17 Q9JKS8 11 23 100.0 119 17 Q9JKS8 13 23 100.0 119 17 Q9JKS8 14 23 100.0 119 17 Q9JKS8 15 23 100.0 119 17 Q9JKS8 16 23 100.0 119 17 Q9JKS8 16 23 100.0 147 16 Q8X935 16 23 100.0 147 16 Q8X935 16 23 100.0 147 16 G8X5E6

Gaps

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RESULT 1

P82341

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SEQUENCE FROM N.A. Schulte U., Asjan V., Hoheisel J., Brandt P., Fartmann B., Holland R., Schulte U., Asjan V., Hoheisel J., Brandt G., Mewes H.W., Mannhaupt G., Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                               Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CML029 from USA."; Nucleic Acids Res. 28:2311-2314 (2000).

EMBL; AR001651; AAD18834.1; "BMBL; AR002547; BAAD1883-1; "BMBL; AR002547; BAAD1884-1; "BMBL; AR002547; BAAD1884-1; "BMBL; AR002547; BAAD1884-1; "BMBL; AR002547; BAAD1884-1; "BMBL; AR002547; BAAD1887-1; "BMBL; AR002547; BAAD1887-1; "BMBL; AR002547; BAAD1887-1; "BMBL; AR002547; BAAD1887-1; "BMBL; AR002547; BAAD1887-1; "BMBL; AR002547; BAAD1887-1; "BMBL; AR002547; BAAD1887-1; "BMBL; AR002547; BAAD1887-1; "BMBL; AR002547; BAAD1887-1; "BMBL; AR002547; BAAD1887-1; "BMBL; AR002547; BAAD1887-1; "BMBL; AR002547; BAAD1887-1; "BMBL; AR002547; BAAD1887-1; "BMBL; AR002547; BAAD1887-1; "BMBL; AR002547; BAAD1887-1; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBR; AR002547; "BMBL; AR002547; "BMBL; AR002547; "BMBL; AR002547; "
   Olinger L., Grimwood J., Davis R.W., Stephens R.S., "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."; Nat. Genet. 21:385-389(1999).
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Eukaryota; Pungi, Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 23; DB 16; Length 50; 100.0%; Pred. No. 2.4e+02;
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Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL513463; CACC2979.2; -.
InterPro; IPR001901; SecB.
InterPro; IPR004795; SecB_euk_arch.
Prom; PD010355; SecB_euk arch; 1.
TIGRFAMS; TIGR00327; SecB_euk arch; 1.
PROSITE; PS01067; SECB_EGE euk arch; 1.
PROSITE; PS01067; SECB_EGEGI; UNKNOWN_1.
PHypochetical protein.
SEQUENCE 70 AA; 7809 MW; ED4EC64FE6B2B9BC CRC64;
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; Pred. No. 3.2e+02;
0; Mismatches 0; Indels
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
Hypothetical 7.8 kDa protein.
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01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
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                                                                                                                                                                                                             MEDLINE=20330349; PubMed=10871362;
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ilarity 100.0%;
Conservative 0
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Best Local Similarity
Matches 5; Conserv
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7 EILDV 11
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Q9C2D4;
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Q9C2D4
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Q8ulr6 pyrococcus
Q99mdl cricetulus
Q9r0e0 rattus norv
Q86693 mus musculu
Q937y3 edwardsiell
Q66448 aquifex aeo
Q6843 arabidopsis
Q8twg7 methanopyru
Q9d3y6 mus musculu
Q55864 synechocyst
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids I, Fabales, Fabaceae, Papilionoideae, Vicieae, Pisum.
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MEDLINE=20181728; PubMed=10715320;
Peltier J. D.B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,
Adamska I., van Wijk K.J.;
"Protecomics of the chloroplast: systematic identification and
targeting analysis of lumenal and peripheral thylakoid proteins.";
Plant Cell 12:319-341(2000).
--- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEAVES.
THIS UNKNOWN
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MEDLINE=99206606; PubMed=10192388;
Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2000 (TrEMBLrel. 14, Created)
01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Unknown protein from 2D-page of thylakoid (SPOT251) (Fragment).
Pisum sativum (Garden pea).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF
PROTEIN IS: 8.5, ITS MW IS: 16.9 KDA.
Chloroplast; 714 14 14
NON TER
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 14 AA; 1590 MW; 6D968D2994D0185B CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
91-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein CPn0685.
CPN0685 OR CPJ0685.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 AA
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                                                                     Q9R0E0
088693
Q937Y3
066448
Q9SZ37
Q8TWG7
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Q55864
   Q8U1R6
Q99MD1
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Best Local Similarity 100.
Matches 5; Conservative
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      NCBI_TaxID=3888;
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7 EILDV 11
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P82341;
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SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=TESTIS;
MEDLINE=21085660; PubMed=11217851;
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Best Local Similarity
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09JKS2
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                                                                                                                                                                                                                                                                                                               Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A., Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.; "Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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                                                                                                      Bacteria, Firmicutes; Bacillus/Clostridium group; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
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100.0%; Pred. No. 4.1e+02;
iive 0; Mismatches 0; Indels
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01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Probable cell division topological specificity factor.
MINE OR CPE2137.
                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
EMBL, AP003193; BABB1843.1; --
Cell division; Complete proteone.
SEQUENCE 90 AA; 10129 MW; P881B16F95880ACD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
11-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 10.3 kDa protein.
Pseudomonas putida.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Conservative
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                                                                                       Clostridium perfringens.
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4930568L21RIK.
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Beet Local Similarity
5, Conserv?
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=13 / TYPE A;
PubMed=11792842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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NCBI_TaxID=303;
                                                                                                                                                                                                                                                                                                                                                                                                         flesh-eater.";
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08 VMP3
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RA Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y., Ra Arakawa T., Hara A., Shibata K., Konno H., Adachi J., Fukuda S., Radawa T., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., A Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Satto R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Pleischmann W., Gasterland T., Gissi C., King B., Kochiwa H., Rachel P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Magner L., Washio T., RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., R. Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., A Gustincich S., Hill D., Hofmann M., Mume D.A., Kamiya M., Lee N.H., Kondone P., Ring B., Ringwald M., Razarelli J., Sakamoto N., RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., A Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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01-OCT_2000 (TrEMBLrel. 15, Last sequence update)
01-OCT_2000 (TrEMBLrel. 15, Last sequence update)
01-OCT_2000 (TrEMBLrel. 15, Last annotation update)
Mutant c-kit receptor (Fragment).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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STRAIN=BROWN NORWAY; TISSUE=TESTIS;
Gangadharan S., Ali S.;
"RT-PCR generated mRNA transcript from proven infertile Brown Norway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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Submitted (JAN 2000) to the EMBL/GenBank/DDBJ databases
EMBL; AF228308; AAF69131.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBI, AKO16255; BAB30165.1; -.
MGD; MGI:1923108; 4930568L21Rik.
SEQUENCE 100 AA; 11528 MW; 59CFB27CD19C1112 CRC64;
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116 116
116 AA, 12583 MW, 8BDASFB24E2471EC CRC64;
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nes 5; Conservative
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STRAIN=VC-16 / DSM 4304 / ATCC 49558;

STRAIN=VC-16 / DSM 4304 / ATCC 49558;

MEDLINE=98049343; PubMed=9389475;

Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

Kletchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,

Richardson D.L., Kerlavage A.R., Graham D.B., Kyrpides N.C.,

Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,

Fleischmann R.D., Quackenbush A., McKenney K., Adams M.D., Loftus B.,

Feterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,

Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,

Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,

Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,

Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                 "RT_PCR generated mRNA transcript from proven infertile Brown Norway male rat testis.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 100.0%; Score 23; DB 11; Length 117; Local Similarity 100.0%; Pred. No. 5.2e+02; les 5; Conservative 0; Mismatches 0; Indels C
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                                                                                                                                                                                                                                                                                                                                                                                                                                 117 117
117 AA; 12641 MW; F3FBDC2F1288F378 CRC64;
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119 AA; 14025 MW; 7F75DA993E80C15C CRC64;
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Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobacea; Archaeoglobus.
NCBI_TaxID=2234;
Q9JKR8;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0JAN-1998 (TrEMBLrel. 05, Created)
01-0JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein AF1530.
                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-BROWN NORWAY; TISSUE=TESTIS;
Gangadharan S., Ali S.;
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InterPro; IPR003600; Ig_like.
SMART; SM00410; IG_like; 1.
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EMBL, AE000997, AAB89718.1; -.
TIGR, AF1530; -.
                                                                                C-kit receptor (Fragment).
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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"RT-PCR generated mRNA transcript from proven infertile Brown Norway
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"RT-PCR generated mRNA transcript from proven infertile Brown Norway
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                                                                                                                                                                                                                                                                                                          male rat testis.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF228307; AF769130.1; -.
InterPro; IFR03500; Ig_like.
SMART; SM00410; IG_like; 1.
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Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF228309; AF669132.1; -.
InterPro; IFR03600; Ig_like.
SWART; SM00410; IG_like; 1.
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117 117
117 Aa; 12635 MW; E2141AF47115EE78 CRC64;
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117 117
117 AA, 12611 MW, E7BEC87E579CB678 CRC64;
                                  01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2001 (TrEMBLrel. 18, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                              STRAIN=BROWN NORWAY; TISSUE=TESTIS, AND BRAIN;
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    117 AA
    PRT;
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                                                                                                    C-kit receptor (Fragment).
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PRELIMINARY;
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                     Q9JKS2;
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RESULT 10 Q9JKR8 ID Q9JKR8

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STRAIN=015:H7 / RIMD 0509952;
MEDLINE=21156211; PubMed=11258796;
MEDLINE=21156211; PubMed=11258796;
MEDLINE=21156211; PubMed=11258796;
Han C.-G., Ohtesubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiha T., Hattori M., Shinagawa H.,
"Complete genome sequence of enterochemorrhagic Escherichia coli
"Complete genome sequence of enterochemorrhagic secherichia coli
0157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=CT18;
MEDLINE=21534947; PubMed=11677608;
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
Nature 409:529-533(2001)
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SEQUENCE FROM N.A.

STRAIN-0157.H7 / EDL933 / ATCC 700927;

MEDLINE-21074935. PubMed=1120651;

Perna N.T., Plunket G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Rose D.J., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Melch R.A., Blattner F.R.,
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                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNA-2002 (TrEMBLrel. 21, Last annotation update)
Putative PTS enzyme II B component.
YADI OR ECS0131.
Escherichia coli 0157:H7.
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Last annotation update)
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Archaea; Buryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
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Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0
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STRAIN=VC1 / DSM 3638 / ATCC 43587 / JCM 8422;
Weiss R.B., Dunn D.M., Robb P.T., Brown J.R.;
"The complete sequence of the Pyrococcus furiosus genome.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE010189; AAL80810.1;
Hypothetical protein; Complete protecome.
SEQUENCE 139 AA: 16222 MW; 0879C8B7133FCE1A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Halobacterium sp. (etrain NRC-1).
Archaea, Euryarchaeota, Halobacteria, Halobacteriales,
Halobacteriaceae, Halobacterium.
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SEQUENCE 119 AA; 13648 MW; 585905ABA983B9B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                               01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2001 (TrEWBLrel. 16, Last annotation update)
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Best Local Similarity
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                                                                                                 109 EILDV 113
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F., Prensier G., Barbe V., Peyretaillade E., Brottier P., Wincker P. Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M., Weissenbach J., Vivares C.P., "Genome sequence and gene compaction of the eukaryote parasite Encephalitozoon cuniculi.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stransberg R.;
Stransberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC023062; AAH23062.1; -.
Hypothetical protein.
SEOUENCE 159 AA; 18896 MW; 349F26D187132A15 CRC64;
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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EMBL, ALS90445; CAD26668.1; -.
Hypothetical protein.
SEQUENCE 163 AA; 18931 MW; 3A36178CB48421FF CRC64;
                                                                                                                                                                                                                                                                                                            01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypotherical 18.9 kDa protein.
Mus musculus (Mouse)
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01-UUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Pred. No. 6.9e+02;
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100.0%; Score 23; DB
Best Local Similarity 100.0%; Pred. No. 6.9
Matches 5; Conservative 0; Mismatches
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Hypothetical protein ECUOS_1480.
ECUOS_1480
Encephalitozoon cuniculi.
                                                                                                                                                                                                                                                     PRELIMINARY;
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QBR1U7;
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Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
Cronin A., Davies P., Davies R.M., Dowd L., White N., Farrar J.,
Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
A Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
Mhitchead S., Barrell B.G.;
T. Complete genome sequence of a multiple drug resistant Salmonella
T. T. T. A. A. B. Sellon J.,
T. T. A. Mature 413:848-852(2001).
T. BEBL; AL627273; CAD02501.1;
T. BEBL; AL627273; CAD02501.1;
W. Hypothetical protein; Complete proteome.
W. SEQUENCE 147 AA; 16938 MW; 70844C913F9CC8A4 CRC64;
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STRAIN=CDC 1551 / OSHKOSH;
STRAIN=CDC 1551 / Jand D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Haft D., Hickey E.,
Feterson J., DeBoy R., Dodson R. Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
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MEDLINE=9829987; PubMed=9634230;

Gordon S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,

Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,

Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,

Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

Oliver S., Geeger K., Skelton S., Squares S., Squares R.,

Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

Deciphering the biology of Mycobacterium tuberculosis from the

Complete genome sequence.";
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"Whole genome comparison of Mycobacterium tuberculosis clinical and
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL022004; CAA17660.1; -.
EMBL; AE006976; AAK45118.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JURA-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein Rv0854.
RV0854 AR WRV043.47 OR WT0877.
Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteridae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MMBL; ALV.
TIGR; MT0877; -.
Tuberculist; Rv0884; -.
Hypothetical protein; Complete proteome.
Hypothetical 147 AA; 16345 MW; D8B55F6B86293E07 CRC64;
TOTHER TAY AB; 16345 MW; D8B55F6B86293E07 CRC64;
TOTHER TAY AB; Lengt
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MEDLINE=21534947; PubMed=11677608;

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Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,

Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,

Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,

Cronin A., Davis P., Davies R.M., Dowd L., White N., Parrar J.,

Reltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,

Reltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,

A graph A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,

Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,

Whitehead S., Barrell B.G.;

"Complete genome sequence of a multiple drug resistant Salmonella

"In neterica serovar Typhi CT18.";

"Nature 413:848-852(2001).

REMBL; AL627267; CAD05018.1; -.

REMBL; AL627267; CAD05018.1; -.

REMBL; AL627267; All AIR_Carboxyl.
                                                                                                                                                                                                                                                                                                                                                                                                                     Salmonella typhi.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriacese;
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Ding D.Q., Tomita Y., Yamamoto A., Chikashige Y., Haraguchi T.,
Hiraoka Y.;
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                    Length 169;
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1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Phosphoribosylaminoimidazole carboxylase catalytic subunit.
                                                              IndelB
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Splitosaccharomyces pombe (Fission yeast).
Sukarycia: Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetales;
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Last annotation update)
100.0%; Score 23; DB 16; Conservative 0: Mismatch.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence
01-DEC-2001 (TrEMBLrel. 19, Last annotati
Hypothetical nuclear protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00731; AIRC; 1.
TIGRFAMB; TIGR01162; purE; 1.
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Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=601;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUA-2002 (TrEMBLrel. 21, Last annotation update)
Phosphoribosylaminoimidazole carboxylase = AIR carboxylase, catalytic subunit (EC 4.1.1.21).
PURE OR STM0534.
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MEDLINE=21534948; PubMed=11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan B., Sun H., Florae L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;

"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                    Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
Methanopyrus.
NCBI_TaxID=2320;
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EMBL, AE010311; AAM01336.1;
Lyase; Pyruvate; Complete proteome.
SEQUENCE 164 AA; 19130 MW; 02861FCDE99CB69D CRC64;
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Salmonella.
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                                                                                                                                                                 01-UUN-2002 (TrEMBLrel. 21, Created)
01-UUN-2002 (TrEMBLrel. 21, Last sequence update)
01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
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UBIC OR MKO119.
Methanopyrus kandleri.
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STRAIN-AV19 / DSM 6324 / JCM 9639;
MEDLINE=21927647; PubMed=11930014;
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InterPro.; PRR000031; AIR_carboxyl.
Pfam; PF00731; AIRC; 1.
TIGRFAMs; TIGR01162; purE; 1.
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SEQUENCE 169 AA; 17794
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Matches 5; Conservative
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                    27 EILDV 31
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Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
Bennett G.N., Koonin E.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-producing
J. Bacterium Clotridium acetobutylicum.";
J. Bacteriol. 183:4823-4838(2001).

EMBL; AB007683; AAK79705.1; -.
                                                                                                                                                                                                                                                                                                               100.0%; Score 23; DB 16; Length 174; larity 100.0%; Pred. No. 7.5e+02; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                        174 AA; 20244 MW; 80EA9CA386E436BF CRC64;
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les 5; Conserv
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es 5; Conserv
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Matches
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Q8ZC15
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"Large-scale screening of intracellular protein localization in living fisation yeast cells by the use of a GFP-fusion genomic DNA library."; Genes Cells 5:169-190(2000).

EMBL, AB027955; BAA87259.1; -.
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Bukaryota, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                  100.0%; Score 23; DB 3; Length 171; 100.0%; Pred. No. 7.3e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 172;
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100.0%; Pred. No. 7.4e+02;
"" "" "" or Indels
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FlyBase; FBgn0044817; Ste12DOR.
InterPro; IPR00704; CAS kinase_II.
Pfam; PF01214; CK_II bela; 1.
PRINTS; PR00472; CASNKINASEII.
PROSITE; PS01101; CK2_BETA; 1.
SEQUENCE 172 AA; 19525 MW; A2C8752F3A976F8B CRC64;
                                                                                                                                                                                                                        171 AA; 21395 MW; 30012B18345508BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0CT-2001 (TrEMBLrel. 18, Last annotation update)
Uncharacterized conserved protein (coiled-coil).
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STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE=21359325; PubMed=11466286;
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Clostridium acetobutylicum.
                                                                                                                                                                                                                                                                                                                                                  5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                             Nuclear protein.
NON_TER 171
NON_TER 171
SEQUENCE 171 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stellate protein.
STE12DOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 EILDV 155
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Q9NIV2
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Methanopyrus kandleri.
Archaea; Buryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
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PROSITE; PSO1128; SHIKIMATE KINASE; UNKNOWN_1.
Kinase; Transferase; Complete proteome.
SEQUENCE 174 AA; 18864 MW; BDSA1E8BF88730D6 CRC64;
Q8ZC15 PRELIMINARY; PRT; 174 AA.
Q8ZC15;
Q8ZC15;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNA-2002 (TrEMBLrel. 21, Last annotation update)
Shikimate_kinase II (EC 2.7.1.71).
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Last annotation update)
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llarity 100.0%; Pred. No. 7.5e+02;
Conservative 0; Mismatches 0;
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InterPro; IPR000623; Shik kinase.
Pfam; PF01202; SKI; 1.
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=CO-92 / BIOVAR ORIENTALIS;
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Wernegreen J.J., Riley M.A.; "Comparison of symbiotic and housekeeping "Comparison of the evolutionary dynamics of symbiotic and housekeeping loci: a case for the genetic coherence of rhizobial lineages."; mol. Biol. Evol. 16:98-113(1999).
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Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
                                                                                                                                                                                                                                                                                                                                 Сарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Streptococcaceae; Streptococcus.
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                                                                                                                                                                                                                                                                           Score 23; DB 2; Length 180;
Pred. No. 7.7e+02;
                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                        SEQÜENCE 180 AA; 19338 MW; 898CCF39389C655A CRC64;
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SEQUENCE 180 AA; 20399 MW; 3898616FB9EEF6E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
10.DEC-2001 (TrEMBLrel. 19, Last annotation update)
Expothetical protein SP1280.
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Last annotation update)
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Pred. No. 7.7e+02;
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01-JUN-2002 (TrEMBLrel. 21, Last seque
01-JUN-2002 (TrEMBLrel. 21, Last annot
DNA-directed RNA polymerase subunit E'
RPOEI OR MK1451.
                                                                                                         EMBL; AF063458; AAD11328.1; -.
InterPro; IPR002509; Polygac_deacet.
Pfam; PF01522; Polygac_deacet; 1.
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EMBL; AE007427; AAK75384.1; -.
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Best Local Similarity 100.0%;
Matches 5; Conservative 0
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                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                         Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N., Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L., Matale D.A., Rogozin I.B., Tatuskin K.L., Wolf Y.I., Stetter K.O., Malykh A.G., Koonin E.V., Kozyawkin S.A., "The complete genome of hyperthermophile Methanopyrus kandleri AV19 and monophyly of archaeal methanogens.";

EMBI, AR010445; AAM02768.1; -. 99:4644-4649(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
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Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, U12643; AAG32547.1; -.
Hypothetical protein.
SEQUENCE 176 AA; 19929 MW; B73E430114725CFF CRC64;
                                                                                                                                                                                                                                                                                                                                                                               Complete protecome.
SEQUENCE 175 Aa; 19325 MW; 695D9BAFFD1AC73B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Nodulation protein B (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 23; DB 17; 100.0%; Pred. No. 7.5e+02;
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MEDLINE=99261640; PubMed=10331255;
                                                                                                      STRAIN=AV19 / DSM 6324 / JCM 9639;
MEDLINE=21927647; PubMed=11930014;
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Best Local Similarity luv...
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                                                                               SEQUENCE FROM N.A.
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                            WCBI_TaxID=2320;
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  Methanopyrus
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RESULT 27
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                             "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum aerophilum.",
                                                                                                                                                                    Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peters S.A., van Staveren M., Dirkse W., Stiekema W., Mewes H.W.,
Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                    Score 23; DB 17; Length 194;
Pred. No. 8.3e+02;
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Bancroft I., Mewes H.W., Mayer K.F.X., Lemcke K., Mannhaupt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:984-989 (2002).
EMBL. AE009904; AAL64578.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 194 AA; 21893 MW; 558DA7CC8AA4BF31 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 2.9 kDa protein.
14C9-40 OR AT4G12200.
Arabidopsis thaliana (Mouse-ear cress).
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                                                         [1]
SEQUENCE FROM N.A.
CHINTALTM2 / ATCC 51768 / DSM 7523;
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Pfam; PF000098; zf-CCHC; 1.
SMART; SM00143; Znf CZHC; 1.
Hypothetical protein.
Thermoproteaceae; Pyrobaculum.
NCBI_TaxID=13773;
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Best Local Similarity 100.0%;
Matches 5; Conservative 0
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                                                                                                                               Slearev A.I., Mazhevaya K.V., Makarova K.S., Polushin N.N., Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L., Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O., Malykh A.G., Koonin E.V., Kozyavkin S.A., Wolf Y.I., Stetter K.O., malykh A.G., Koonin E.V., Kozyavkin S.A., Wolf Y.I., Stetter K.O., "The complete genome of hyperthermophile Methanopyrus kandleri AV19 and monophyly of archaeal methanogens."; Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649 (2002).

Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649 (2002).

BNBL, AB010437; AAM02664.1;

DNA-directed RNA polymerase; Complete proteome.

SEQUENCE 183 AA; 20754 MW; C43AA6784B63750D CRC64;
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
NCBI_TaxID=9913,
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Archaea, Crenarchaeota, Thermoprotei, Thermoproteales,
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Fibronectin variable region (Fragment).
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
Hypothetical protein PAE2972.
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                                                                                STRAIN=AV19 / DSM 6324 / JCM 9639;
MEDLINE=21927647; PubMed=11930014;
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EMBL; AF260305; AAF91381.1; -.
InterPro; IPR003961; FN_III.
Pfam; PF00041; fn3; 1.
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  NCBI_TaxID=2320;
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56 EILDV
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Q9MZ31
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1D 082U3
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Debelle F., Plazanet C., Roche P., Pujol C., Savagnac A.,
Rosenberg C., Prome J.C., Denarie J.;
Rosenberg C., Prome J.C., Denarie J.;
The Noda proteins of Rhizobium meliloti and Rhizobium tropici specify
the N-acylation of Nod factors by different fatty acids.";
Mol. Microbiol. 22:303-314(1996).
EMBL, X98514; CAA67138.1; -.
EMBL, PSO19519; Polysac deacet.
Plan, PPO1522; Polysac deacet.
Pfan, PRO1522; Polysac deacet.
SEQUENCE 219 AA; 23566 MW; 7394719AFFB1743C CRC64;
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MEDLINE-99287316; PubMed=10360571;
Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.C., Ketchum K.A.,
Haft D.H., Hickey B.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G., Pleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Vonter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
Mature 399:323-329(1999).
EMBL; AR001708; AAD35348.1; -.
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Gaps
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Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
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Rhizobiaceae; Rhizobium.
NCBI_TaxID=398;
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Pred. No. 9.2e+02;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein TM0260.
                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Pfam; PF01865; DUF47; 1.
Hypothetical protein; Complete proteome.
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Best Local Similarity 100.0%;
Matches 5; Conservative 0;
5; Conservative
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Kullman S.W., Mateumura F.;

"Identification of a novel cytochrome P-450 gene from the white rot fungue Phanerochaete chrysosporium.";

-1- Siwilcariy: Bicolos To THE CYTOCHROWE P450 FAMILY.

EMBL; AF005475; AAB63277.1; -...

Interbro; IPR01128; Cytochrome_P450.

Pfan; PR00667; P450;

PRINTS; PR00385; P450.

PRINTS; PR00386; CYTOCHROME_P450; 1.
                                                                                                                                                                                       Cytochrome P450 (Fragment).
CYP63-1A.
Phanerochaete chrysosporium.
Bukaryota, Fungi, Basidiomycota, Hymenomycetes, Homobasidiomycetes;
Aphyllophorales; Corticiaceae, Phanerochaete.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 23; DB 3; Length 208; 100.0%; Pred. No. 8.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Godfrey H.P., Ebrahim A.A.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
EMBL, TA1850; ADMO0014.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212
23232 MW; B3741B219D6pB631 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208 AA; 24096 MW; 8254CD4F1CC668C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
                                                                                                                                                      (TrEMBLrel. 05, Last sequence update) (TrEMBLrel. 20, Last annotation update)
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Pred. No. 9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212 AA
                                                                               208 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Heme; Monooxygenase; Oxidoreductase.
NON_TER 1
                                                                                                                                Created)
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InterPro; IPR003961; FN_III.
Pfam; PF00041; fn3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97355939; PubMed=9212420;
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01-MAY-1999 (TrEMBLrel. 10, Le
01-DEC-2001 (TrEMBLrel. 19, La
Fibronectin (Fragment).
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                                                                                                                             01-JAN-1998 (TrEMBLrel. 05,
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hes 5; Conservative
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                                                                            PRELIMINARY;
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212 AA;
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Best Local Similarity
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SEQUENCE
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RESULT 35 095609

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CRAINE-DELTA H;

KREDLINE-98037514; PubMed-9371463;

KREDLINE-98037514; PubMed-9371463;

MEDLINE-98037514; PubMed-9371463;

Addredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,

A Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,

Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,

A Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,

A McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,

Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;

"Complete genome sequence of Methanobacterium thermoautotrophicum

T deltaH: functional analysis and comparative genomics.";

J. Bacteriol. 179:7135-7135-115.

REMBL; AB000887; AAB85681.1; -.
     "The genome of the natural genetic engineer Agrobacterium tumefaciens ^{-5}G8 ":
                                                                                                             SECUENCE FROM N.A.

MEDLINE=21608551; PubMed=11743194;
Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Goodner B., Hinkle G., Cattung S., Miller N., Halling C., Mullin L.,
Qurollo B., Goddman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
Gielo C., Slater S.,
"Genome sequence of the plant pathogen and biotechnology agent
Agrobacterium tumefaciens C58.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 23; DB 17; Length 242; 100.0%; Pred. No. 1e+03; 1.ve 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Archaea; Buryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein; Complete proteome.
SEQUENCE 231 AA; 25246 MW; 59110EA68CE538AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 AA; 26475 MW; 8CBC1A2252AE70E2 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 100.0%; Score 23; DB 16; Similarity 100.0%; Pred. No. 9.7e+02; 5; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
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                                                                                                                                                                                                                                                                                                                                                                                  Science 294:2323-2328(2001).
                                                                      Science 294:2317-2323(2001).
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01-JAN-1998 (TrEMBLrel. 05,
01-JAN-1998 (TrEMBLrel. 05,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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Matches 5; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conserved protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=187420;
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Beudomonas fluorescens BL915.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF23768; AFF61718.1;
InterPro; IPR001690; Autoind synth.
PRINTS; PR01549; Autoind synth; 1.
PRODM; PR002752; Autoind synth; 1.
PROSITE; PS00949; AUTOINDÜCERS SYNTH; 1.
SEQUENCE 226 AA; 25692 MW; 99D340438EE95B3D CRC64;
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Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
Chen Y., Paulsen I.T., Eisen Jah., Karp P.D., Bovee D. Sr.,
Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
Zhang G., Yoo H., Tao Y., Biller P., Jung M., Krespan W., Perry M.,
Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                   Gaps
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
Hypothetical protein Atu3494.
ATU3494 OR AGR L. 2665.
Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria, Proteobacteria, alpha subdivision, Rhizobiaceae group;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
NCBI_TaxID=294;
                                            100.0%; Score 23; DB 16; Length 222; 100.0%; Pred. No. 9.4e+02;
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                                                                                                0; Indels
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22E680FFB3CB3B52 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Putative acylhomoserine lactone synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 23; DB 2; I
100.0%; Pred. No. 9.5e+02;
iive 0; Mismatches 0;
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                                                                                                0; Mismatches
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222 AA; 25926 MW;
                                                                      Best_Local Similarity 100.
Matches 5; Conservative
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les 5; Conserv
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SEQUENCE
                                              Query Match
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Q91606
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DR ERMBL;
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MEDLINE=98065943; PubMed=9403685;
Praser C.M., Cagiens S., Huang W.M., Sutton G.G., Clayton R.A.,
Praser C.M., Cagiens S., Huang W.M., Sutton G.G., Clayton R.A.,
Dougherty B., Tomb J.-P., Relschmann R.D., Richardson D.,
Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
Utterback T., Matthey L., McDonald L., Artlach P., Bowman C.,
Garland S., Fujii C., Cotton M.D., Horet K., Roberts K., Hatch B.,
Smith H.O., Venter J.C.;
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Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genomic sequence of a Lyme disease spirochaete, Borrella
    Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR003743; DUF164.
Pfam; PF02591; DUF164; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 253 AA; 29838 MW; 20169A5790F824E1 CRC64;
                                                                                                                                                                                                                                                                                                                                          Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetacese, Borrelia.
                                                                                                                                                                                               01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
BHypothetical protein BB0713.
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Last annotation update)
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      Mismatches
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MEDLINE=94150718; PubMed=7906398;
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01-JUN-1998 (TrEMBLrel. 06, L6
01-DEC-2001 (TrEMBLrel. 19, L6
H10D12.2 protein.
H10D12.2.
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EMBL; AE001171; AAC67060.1;
TIGR; BB0713; -.
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      Conservative
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Matches 5; Conserv
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SEQUENCE FROM N.A.
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CTRAIN=0157:H7 / RIMD 0509952;

X MEDLINE-21156231. PubMed=11258996;

A Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., R. Inda T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., R. Anibara S., Shiba T., Hattori M., Shinagawa H.;

ROmplete genome sequence of enterohemorrhagic Escherichia coli

RT O157:H7 and genomic comparison with a laboratory strain K-12.";

REMBL; AR00545; AAGS7376.1;

DR EMBL; AR005501; BAB36553.1;

DR EMBL; PR00500; HpCH-HpaI;

DR Ffam; PF03328; HpCH-HpaI;

DR Ffam; PF03328; HpCH-HpaI;

DR Ffam; PF03328; HpCH-HpaI;

DR Ffam; PF03328; HpCH-HpaI;

DR Ffam; PF03328; HpCH-HpaI;

DR Ffam; PF03328; HpCH-HpaI;

DR Ffam; PF03328; HpCH-HpaI;

DR Ffam; PF03328; HpCH-HpaI;
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                                                                                                                                             Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
Lactobacillaceae; Lactobacillus.
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Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-0157-H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
MEDLINE=21074935; PubMed=11206551;
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Agctbeck B.J., Davis N.W., Lim A., Dimalanta R.T., Potamousis K., Apodaca J., Anancharama T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                423FFFC817975600 CRC64;
O9FDJ6;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Hypothetical 28.8 kDa protein.
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Last annotation update)
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Z3503 OR ECS3130.
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Matches 5, Conservative
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                                                                                                                             Lactobacillus rhamnosus
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Best Local Similarity
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                                                                                                                                                                                         NCBI_TaxID=47715;
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SEQUENCE 250 AA
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PRELIMINARY;
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Q97WL9
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Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R., Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.; "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=1021;

MEDLINE=21366509; PubMed=11481432;

Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,

Barnot-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,

Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,

Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,

Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;

'"Nucleotide sequence and predicted functions of the entire

Sinorhizoblum melliolty bysymA megaplasmid.";

Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888 (2001).
                                                                                                                                                                                                                                                                                Gaps
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DT-2002 (TrEMBLrel. 19, Last annotation update)
Nitrate transport ATP binding protein, probable.
RA0305 OR SMA0581.
RA0305 OR SMA0581.
Plasmid pSyma (megaplasmid 1).
Plasmid pSyma (megaplasmid 1).
Bacteria, Proteobacteria; alpha subdivision, Rhizobiaceae group,
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                                                                                                                                                                                                                                                        Length 256;
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100.0%; Pred. No. 1.1e+03;
tive 0; Mismatches 0; Indels
                                                                                                                       Ozersky P.;
"The sequence of C. elegans cosmid H10D12.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                           Waterston R.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF038620; AAB93487.1; -.
SEQUENCE 256 AA; 28085 WW; B93E1E6AFA44CD3B CRC64;
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Pfam; PF00005; ABC tran; 1.
ProDom; PD000006; ABC transportr; 1.
TIGRPAMS; TIGR01184; ntrCD; 1.
PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.
Plasmid; Complete proteome.
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Best Local Similarity 100.00
Then 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                          Nature 368:32-38(1994).
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EILDV 227
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STRAIN=ATCC 35092 / DSM 1617 / P2;
STRAIN=21332956; PubMed=11427726;
She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Cuxtis B.A.,
De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
Heikamp-de Jong I., Jeffrids A.C., Kozera C.J., Medina N., Peng X.,
Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
"The complete genome of the crenarchecon Sulfolobus solfataricus P2.";
Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
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Verma P.K., Kumar V., Singh P.K., Upadhyaya K.C.;
"Isolation of a cDNA clone encoding a putative Hslpro-1 homolog from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                 Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae; Sulfolobus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 100.0%; Score 23; DB 10; Length 268; Similarity 100.0%; Pred. No. 1.1e+03; 5; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chickpea.";
Submirted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; ATO 20680; AAK72104.1; -
SEQUENCE 268 AA; 30773 MW; A91E326F80E108CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267 AA; 29663 MW; F485C1E07E92674A CRC64;
                                   01-0CT-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0TW-2002 (TrEMBLrel. 21, Last annotation update)
Erythrocyte band 7 membrane protein homolog.
8S02195.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Putative Hsipro-1-like protein.
Cicer arietinum (Chickpea) (Garbanzo).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEAM; PF01145; Band 7; 1.
PRINTS; PR00721; STÖMATIN.
SMART; SM0244; PHB; 1.
Complete proteome.
SEQUENCE 267 AA; 29663 MW; F485CIE07E92674A CRO
267 AA.
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PRT;
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Interpro; IPR001107; Band 7.
InterPro; IPR001972; Stomatin.
InterPro; IPR000531; TonB_boxC.
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STRAIN-BROWN NORWAY, TISSUB-TESTIS;
Gangddharan S., Ali S.;
Gangddharan S., Ali S.;
Gangddharan S., Ali S.;
Gangddharan S., Ali S.;
Gangddharan S., Ali S.;
Gangddharan S., Ali S.;
Submitted M.G. 2000) to the EMBL/GenBank/DDBJ databases.
BMBL, AR296694, AR468585.1;
InterPro; IPR003609; Ig_like.
SWART; SM00410; IG_like; 1.
                                                                                                                                                                                                 01-47.2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MUN-2001 (TrEMBLrel. 17, Last annotation update)
01-UUN-2001 (Tremmert).
C-kit receptor (Fragment).
Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 23; DB 11; Length 274;
Pred. No. 1.1e+03;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2002 (TrEMBLrel. 21, Last annotation update)
Similar to Dand (Hsp40) homolog, subfamily B, member 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON TER 274 274 SEQUENCE 274 AM; 000FA042B09D0103 CRC64;
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277 AA; 30675 MW; 6D9198A5C4FA1DA3 CRC64;
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                                                                                                                                                                                PRT;
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InterPro; IPR002950; Josephin.
InterPro; IPR003903; UIM.
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Best Local Similarity 100.v
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Pfam; PF02809; UIM; 2.
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                                           251 EILDV 255
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69 EILDV 73
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Q9EQ23;
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0921S2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Segura A., Bunz P.V., D'Argenio D.A., Ornston L.N.;
"Genetic analysis of a chromosomal region containing vanA and vanB, genes required for conversion of either ferulate or vanillate to protocatechuate in Acinetobacter.";
J. Bacteriol. 181:3494-3504(1999).
-i- SIMILARITY: BELONGS TO THE ICLR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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InterPro; IPR000285; HTH_ICIR.
Pfam, PF01614; ICIR, 1.
SWART; SM00346; HTK, 1.
DNA-binding; Hypotherical protein; Transcription regulation.
SEQUENCE 270 AA; 30524 MW; DB457B57BF817FBC CRC64;
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100.0%; Score 23; DB 4; Length 271;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 5; Conservative 0; Mismatches' 0; Indels
                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae; Acinetobacter.
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InterPro; IRRO11919; Znf CCHC. Pfam; PRO0098; zf-CCHC, 4.
Pypochetical protein. Submar; SM00343; Znf CCHC, 4.
Hypochetical protein. 30477 MW; D68EDABE8B9D0F3D CRC64;
                                                                                                                                                                                                                            01-JNN-1998 (TrEMBLrel. 05, Created)
01-JNN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 30.5 kDa protein.
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                                                                                                                                                                                   PRT;
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Best Local Similarity 100.v.
Si Conservative
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Homo sapiens (Human).
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TISSUE=AMYGDALA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                           156 EILDV 160
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| S0 EILDV 54
1 EILDV 5
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STRAIN-C2A / ATCC 35395 / DSM 2834;

STRAIN-C2A / ATCC 35395 / DSM 2834;

MEDLINE-21929760; PubMed-1193238;

Galagan J.E., Nusbaum C., Fory A., Endrizzi M.G., Macdonald P.,

FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,

Allen N. Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,

Linton L., McEwan P., McKernan K., Talraellano K., Johnson R.,

Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,

Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,

Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Ohta S., Yohda M., Ishizuka M., Hirata H., Hamamoto T.,
Otawara-Hamamoto Y., Matsuda K., Kagawa Y.;
Sequence and over-expression of subunits of adenosine triphosphate synthase in thermophilic bacterium PS3.";
Biochim. Biophys. Acta 933:141-141(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=87137359; PubMed=2880841;
Kagawa Y., Ishizuka M., Salahu T., Nakao S.;
"Stable structure of thermophilic proton ATPase beta subunit.";
J. Blochem. 100:923-934 (1986).
EMBL; X07804; CAA30654.1; -.
EMBL; X04609; CAA30655.1; -.
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                                                                                                                                                                                                                                             thermophilic bacterium PS3.
Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales.
NCBI_TaxID=2334;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FA17CE9482EEE9F7 CRC64;
                                                                                                                                            OS2412; O56245; O52409; 01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                               282 AA
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TIGREAMS; TIGRO1146; ATPBYN FYGamma; 1.
PROSITE; PSO0153; ATPASE GAMMA; 1.
SEQUENCE 282 AA; 31778 WW; FAITCE94!
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
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nes 5; Conservative
                                                                                                                             PRELIMINARY;
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EILDV 10
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Springer T.A., Umayam L.A., White O., White R.H., de Macario B.C., Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I., Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander B., Metcalf W.W., Birren B., "The genome of Methanosarcina acetivorans reveals extensive metabolic and physiological diversity.", Genome Res. 12:532-542(2001).
                                                                                                                                                                                                                                                                                                       Gaps
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NCBI_TaxID=6239;
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Pasteurella.
                                                                                                                                                                                                                                                          Length 285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 23; DB 16; Length 287; 100.0%; Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                           Complete proteome.
SEQUENCE 285 AA; 32209 MW, 9AEBDB37DA8868F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical protein PM0569.
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Last sequence update)
Last annotation update)
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MEDLINE=21145866; PubMed=11248100;
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MEDLINE=99069613; PubMed=9851916;
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SORBERTA

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SEQUENCE FROM N.A.

STRAIN=MCS6 / SEROGROUP B;

STRAIN=MCS6 / SEROGROUP B;

MEDLINE=20175755; PubMed=10710307;

Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,

Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,

Nelson W.C., Gwinn M.L., DeBoy R., Petterson J.D., Hickey B.K.,

Haft D.H., Salzberg S.L., White O., Pleischmann R.D., Dougherty B.A.,

Mason T., Ciecko A., Parksey D.S., Blair B., Cittone H., Clark B.B.,

Cotton M.D., Utterback T.R., Khouri H., Oin H., Vamathevan J.,

Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Smith H.O.,

Smith H.O., Fraser C.M., Moxon B.R., Rappuoli R., Venter J.C.,

MCComplete genome sequence of Neisseria meningitidis serogroup B strain
Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S., Jagels K., Leather S., Moule S., Mungall K., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Mhitchead S., Spratt B.G., Barrell B.G.; Strain of Neisseria meningitidis Z2491 "; Marure 404:502-506(2000).

EMBL; ALIG2T55; CAB84611.1; -. InterPro; IPR002500; PAPS reduct.

Pfam; PP01507; PAPS reduct; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neisseria meningitidis (serogroup B).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBI_TaxID=491;
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                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 23; DB 16; Length 307; 100.0%; Pred. No. 1.3e+03; cive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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Transferase; Nucleotidyltransferase; Complete proteome.
SEQUENCE 307 AA; 34696 MW; 4BFF5DB3861D0FD3 CRC64;
                                                                                                                                                                                                                                                                                           Pfam; PF01507; PAPS reduct; 1.
Transferase; Nucleotidyltransferase; Complete proteome.
SEQUENCE 307 AA; 34724 MW; 6D2A1E060C31124C CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Sulfate adenylyltransferase, subunit 2.
NMB1192 AND NMB1154.
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llarity 100.0%; Pred. No. 1.38+03;
Conservative 0; Mismatches 0;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
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Science
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09X9K3;
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Q9JS34
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DT 011
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STRAIN=2019;
PubMed=11842084;
Jones P.A., Samuels N.M., Phillips N.J., Munson R.S. Jr., Bozue J.A., Arseneau J.A., Nichols W.A., Zaleski A., Gibson B.W., Apicella M.A.;
"Haemophilus influenzae Type b Strain A2 Has Multiple
Sialyltransferases Involved in Lipooligosaccharide Sialylation.";
J. Biol. Chem. 277:14558-14611(2002).
EMBL; AY061634; AAL38659.1;
SEQUENCE 304 AA; 36115 MW; 49645B793FPBDF90 CRC64;
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBI_TaxID=65699;
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SEQUENCE FROM N.A.
STRAIN=Z2421 / SEROGROUP A / SEROTYPE 4A;
MEDLINE-20222556; PubMed=10761919;
Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Putative sulphate adenylate transferase subunit 2 (EC 2.7.7.4)
CYSD OR NMA1365.
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Haemophilus.
            "Genome sequence of the nematode C.elegans: A platform for investigating biology."; Science 282:2012-2018(1998).
EMBL; 2815090; CAB04157.1; -.
Interpro; IPR003582; ShKT.
SMART; SM00518; EGF: 1.
SMART; SM00218; EGF; 1.
PROSITE; PS00022; EGF 1; UNKNOWN 1.
SEQUENCE 290 AA; 32686 MW; 700F9BBEllAFRADE
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Last sequence update)
Last annotation update)
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Best Local Similarity 100...
5, Conservative
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01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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RESULT 56
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RESULT 57
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SECUENCE FROM N.A.
TISSUE-BRAIN PARIETAL LOBE;
TOSSUE-BRAIN PARIETAL LOBE;
Osada M., Hida M., Kubuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from macaque brain cDNA
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to protein phosphatase 2, regulatory subunit B (BS6), beta isoform (Fragment).
Mus musculus (Mouse).
Bukaryota, Metacoa; Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NUSI_TAXID=10090;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 35.5 kDa protein.
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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PROSITE; PS0067; KINESIN MOTOR DOMAIN2; 1.
ATP-binding; Coiled coil; Hypothetical protein; Microtubules;
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EMBL; AB047624; BAB12148.1; -.
HSSP; PS6536; 2KIN.
                                                                                                                                                                                                                                 Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 317 Aa; 35489 MW; 28FDC60C4F75A684 CRC64;
                                                                                                                                                                                                                                                                                                         314 AA; 36619 MW; BF6F70007B3E9081 CRC64;
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Pfam; PF00225; kinesin; 1.
PRINTS; PR00380; KINESINHEAVY.
SMART; SM00129; KISC; I.
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1es 5; Conservative
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NCBI_TaxID=9541;
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les 5; Conserv
                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               158 EILDV 162
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SEQUENCE
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Q9GMV1;
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Q97PP0;
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Matches
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Q97PP0
ID Q97PP
AC Q97PPDT 01-OC
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Hilbert H., Duesterhoeft A., Wood V., Rajandream M.A., Barrell B.G.;
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; ALO31907; CAA2142B-1; --
InterPro; IPR001813; 608 ribosomal.
InterPro; IPR001790; Ribosomal L10.
Pfam; PF00428; 608 ribosomal 1.1.
Pfam; PF00466; Libosomal L10; 1.
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                                                                       Vibrio parahaemolyticus.
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 23; DB 2; Length 30
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                     McCarter L.L.;
"Polar Flagellar Region I.";
"Dolar Flagellar Region I.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; U12817; AAA42910.1; -.
HSSP; P06143; 1AB6.
InterPro; IPR002545; CheW.
InterPro; IPR001789; Response_reg.
                                                                                                                                                                                                                                                                                                                                                                                                                       Phosphorylation, Sensory transduction.
SEQUENCE 308 AA; 34126 MW; 5E21A365839BB978 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ribosomal protein.
SEQUENCE 312 AA; 33565 MW; 68979A46B921F761 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales; Schizosaccharomycetaces;
Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1998 (TrEWBLrel. 08, Created)
01-NOV-1998 (TrEWBLrel. 08, Last sequence update)
01-JUN-2001 (TrEWBLrel. 17, Last annotation update)
Putarive 60s acidic ribosomal protein p0.
               01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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                                   Chemotaxis CheV homolog
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Best Local Similarity
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                                                                                                     NCBI_TaxID=670;
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145 EILDV 149
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Q8R342,
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RESULT 60

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Gaps

RESULT 61 Q8R342 ID Q8 AC Q8

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NCBI_TaxID=1902;
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Q9RJ06;
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SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
MEDLINE-21311952; PubMed=11418146;
MEDLINE-21311952; PubMed=11418146;
MIDLINE-21311952; PubMed=11418146;
MIDLINE-21311952; PubMed=11418146;
MIDLINE-21311952; PubMed=11418146;
MIDLINE-21311952; PubMed=11418146;
MIDLINE-21311952; PubMed=1141814, Mosoyama A.,
MIDLINE-21311952; MIDLINE-2131110, Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Puruya K., Yoshino C., Shiba Thattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                         Bacteria, Firmicutes, Bacillus/Clostridium group, Lactobacillales,
Streptococcaceae, Streptococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus aureus (strain Mu50 / ATCC 700699), and Staphylococcus aureus (strain N315).
Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 23; DB 16; Length 321; 100.0%; Pred. No. 1.3e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     321 AA; 35141 MW; FF89A0B001BD8452 CRC64;
01-OCT-2001 (TrEMBLrel. 18, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) Pyridine nucleotide-disulphide oxidoreductase family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAN-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein SAV0553.
SAV0553 OR SA0511.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 321 AA
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InterPro; IPR001327; FAD pyr_redox.
InterPro; IPR001013; PyrIdine_redox_2.
InterPro; IPR01100; Pyr_redox.
Pfam; PF00070; pyr_redox; I.
PRINTS; PR00419; ADXRDTASE.
PRINTS; PR00411; PNDRDTASEII.
                                                                                                                                                                                                                                                           MEDLINE=21357209; PubMed=11463916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 293:498-506(2001).
EMBL; AE007451; AAK75650.1; -.
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NCBI_TaxID=158878, 158879;
                                                                                                           Streptococcus pneumoniae.
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                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                        NCBI_TaxID=1313;
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coelicolor A1(2).",
Nacure 417:141-147(2002).
-!- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES
-!- FUNCTION: THE SIGMA FACTOR IS AN INITIATION SITES AND
ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Redenbach M., Kleser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THEN IS RELEASED (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE SIGMA-70 FACTOR FAMILY. ECF SUBFAMILY.
EMBL; AL109962; CAB53126.1; -.
                                                                                                                                                                                                                                                                                                                                          Gapa
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STRAIN=A3(2) / M145;

Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challie G.L.,

Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challie G.L.,

Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

Thomson N.R., Darwan A., Brown S., Chandra G., Chen C.W., Collins M.,

Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,

Rabbinowitsch E., Rajandram M.A., Rutherford K., Rutter S.,

Rabbinowitsch E., Sanaders D., Squares R., Squares S., Taylor K.,

Marren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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                                                                                                                                                                                                                                                                Length 321;
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Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seeger K.J., Harris D.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases
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Pfam; PF00776; Sigma70 ECF; I.

DNA-binding; DNA-directed RNA polymerame; Sigma factor;

Transcription regulation.

SEQUENCE 322 AA; 35466 MW; C4EEBBA53849677D CRC64;
aureus.";
Lancet 357:1225-1240(2001).
EMBL; AP003359; BAB56715.1; -.
EMBL; AP003130, BAB41742.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 321 AA; 36053 MW; E0B08B19CP630CB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                        100.0%; Score 23; DB 16;
ilarity 100.0%; Pred. No. 1.3e+03;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    322 AA.
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01-UJN-2002 (TrEMBLrel. 21, Last anno
Putative RNA polymerase sigma factor.
SCO0159 OR SCJI.08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                       Local Similarity
168 5; Conserv
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MEDIINE=99120557; PubMed=9923682; Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C., Smith D.R., Ling L.-S.L., Moir D.T., deJonge B.L., Carmel G., Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C., Trust, Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F., Trust T.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genomic sequence comparison of two unrelated isolates of the human
                      "The complete genome sequence of the gastric pathogen Helicobacter pylori";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Putative thioredoxin reductase.
TXRB 2 OR UHP1011.
Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria, Proteobacteria, epsilon subdivision, Helicobacter group,
                                                                                                                                                                                                                                                                                                                                                       Length 324;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gastric pathogen Helicobacter pylori.";

Nature 397:176-180(1999).

Nature 397:176-180(1999).

EMBL; AE001536; AAD06662.1; -

InterPro; IPR0010759; Adrndx_reductase.

InterPro; IPR001017; Pyr_redox.

InterPro; IPR001100; Pyr_redox.

InterPro; IPR001100; Pyr_redox.

InterPro; IPR001100; Pyr_redox.

PRINTS; PR00419; ADXRDTASE.

PRINTS; PR00419; ADXRDTASE.

PRINTS; PR00469; PNDRDTASEI.

PRINTS; PR00469; PNDRDTASEII.

PRINTS; PR00469; PNDRDTASEII.

PRINTS; PR00469; PNDRDTASEII.

PRINTS; PR00469; PNDRDTASEII.

PRINTS; PR00469; PNDRDTASEII.

PRINTS; PR00469; PNDRDTASEII.

PRINTS; PR00469; PNDRDTASEII.

PRINTS; PR00469; PNDRDTASEII.

PRINTS; PR00469; PNDRDTASEII.
                                                                                                                                                                                     InterPro; IPR001327; FAD_pyr_redox.
Pfam; PF00070; pyr_redox; 1.
Hypothetical protein; Complete proteome.
BEQUENCE 324 AA; 35986 MW; 0854598651D92B30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-WAY-1999 (TrEMBLrel. 10, Created)
01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 23; DB 16;
ilarity 100.0%; Pred. No. 1.3e+03;
Conservative 0; Mismatches 0;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
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                                                                                          Nature 388:539-547(1997).
EMBL; AE000622; AAD08209.1;
TIGR; HP1164; -.
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Best Local Similarity
Matches 5; Conserv
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      Venter J.C.;
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Q92K51;
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STRAIN=26695 / ATCC 700392;
MEDLINE=9739467; PubMed=9252185;
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,
Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
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HP1164.

HP1165.

HP11cobacter pylori (Campylobacter pylori).

Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;

Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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0
                                100.0%; Score 23; DB 16; Length 322; 100.0%; Pred. No. 1.3e+03;
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Submitted (JUL.2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC011609; AMH11609.1;
InterPro; IPR001623; DnaJ N.
InterPro; IPR001230; Josephin.
InterPro; IPR001230; Prenyl_site.
InterPro; IPR001230; Prenyl_site.
Pfam; PF00280; JuM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00636; DNAJ 1; UNKNOWN 1.
PROSITE; PS50076; DNAJ 2; 1.
PROSITE; PS00294; PRENTLATION; UNKNOWN 1.
SEQUENCE 324 AA; 35580 MW; 0154ED3E29F34B4A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                           Q96F52;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
DnaJ (H9p40) homolog, subfamily B, member 2.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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100.0%; Pred. No. 1.3e+03;
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Query Match
Beet Local Similarity 100.vv
Theg 5; Conservative
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Best Local Similarity
5, Conserva
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025779
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STRAIN—GSS1 / DSM 4299 / JCM 9571;

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X Rawabhima - T., Amanon N., Kolke H., Makino S.-I., Higuchi S.,

Kawabhima - Ohya Y., Watanabe K., Yamazaki M., Kanehori K., Kawamoto T.,

X Rawabhima - Ohya Y., Watanabe K., Suzuki M.;

Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;

A Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;

Rapence of Thermoplasma volcanium. ", sequence of Thermoplasma volcanium.";

Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).

R EMBL, Appro1991; BAB53307.1; -.

R InterPro; IPR00728; AIRS_related.

R InterPro; IPR00738; PurM_cligase.

Pfam; PF00586; AIRS_r.

R Pfam; PF00586; AIRS_r.

R TIGRPAM; TIGR00878; purM; 1.

R Ligase; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21595265; PubMed=11759840; MEDLINE=21595265; PubMed=11759840; Kuritz T., Sasamoto S., Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Kaneko T., Iriguchi M., Ishikawa A., Kawashina K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Kishida Y., Kohara M., Matsumoto M., Takazawa M., Yamada M., Yasuda M., Tabata S., Sugimoto M., Takazawa M., Yamada M., Complete genomic sequence of the filamentous nitrogen-fixing cyanopacterium Anabaena sp. strain PCC 7120.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 23; DB 16; Length 337;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 5; Conservative 0; Mismatches 0; Indels (
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Thermoplasmataceae; Thermoplasma.
                                                                                                                                                                                                                                                                                                                                                                     Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
       IndelB
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EMBL; AP003588; BAB73886.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 337 AA; 39125 MW; 9E6A546CPEFBF6BB CRC64;
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01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0CT-2001 (TrEMBLrel. 11, Last annotation update)
Phosphoribosylfcarulyglycinamide cyclo-ligase.
TV0165 0R TVG0175535.
                                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
11-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein Alr2187.
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    0; Mismatches
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Q97CD7
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Q8YUZ4
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Klenk H.-P., Clayton R.A., Town J.-F., White O., Nelson K.E.,
Ktenk H.-P., Clayton R.A., Town J.-F., White O., Nelson K.E.,
Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenhush J., Lee N.H., Sutton G.C., Gill S.,
Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
Sadow P.W., D'Andrea K.P., Bowman C., Pujii C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Mature 390:364-370(1997).
EMBL, AE000986, AAB89555.1; --
HSSP, PO8178; ICLI.
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MEDLINE=20500219; PubMed=11048724;
Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,
Cassell G.H.;
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Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
Mycoplasmataceae; Ureaplasma.
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Pred. No. 1.4e+03;
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InterPro; IPRO04733; PurM_cligase.
Pfam; PF00586; AIRS; 1.
Pfam; PF02769; AIRS; 1.
TIGRPAMB; TICRR00878; purM; 1.
Hypothetical protein; Ligase; Complete proteome.
SEQUENCE 329 AA; 36209 MW; C9D291148AE3DD34 CRC64;
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EMBL, AE002107; AAF30482.1; -.

Hypothetical protein; Complete proteome.

SEQUENCE 333 AA; 40137 MW; 39BD610454AD6985 CRC64;
01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Phosphoribosylformylglycinamidine cyclo-ligase (FURM).
                                                                                        Archaea; Buryarchaeota, Archaeoglobi, Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
NCBI_TaxID=2234;
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100.0%; Pred. No. 1.3e+03;
iive 0; Mismatches 0;
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100.0%;
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Best Local Similarity 100...
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                                                                  Archaeoglobus fulgidus.
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01-MAR-2002
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Q9PR68; **09PR68**

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344 AA; 39018 MW; 07B0353EC7F43FFD CRC64;
      Flg_Motor_Flig.
InterPro; IPR000090; Flg_Motor_F
Pfam; PF01706; FliG-C; 1_
PRINTS; PR00954; FLGWOTORFLIG.
TIGRFAM9; TIGR0207; fliG; 1.
Flagella.
SEQUENCE 344 AA, 39018 MW; 0
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8 EILDV 12
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Ge Y., Old I., Saint Girons I., Yelton D.B., Charon N.W.;
"Flith and fill of Borrelia burgdorferi are similar to flagellar and virulence factor export proteins of other bacteria.";
Gene 188:73-75(1996).
EMBL: L76303; AAB51411.1; -.
EMBL; UC9711; AAB514915.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last sequence update)
3-oxoacyl-(acyl carrier protein) synthase III.
Streptomyces avermitilist protein synthase III.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
NCBI TaxID=33903;
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                                                                100.0%; Score 23; DB 17; Length 338; 100.0%; Pred. No. 1.4e+03;
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Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
   338 AA; 37183 MW; 0AC488696971DEF5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia
NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                    339 AA
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                                                                                                                                    0, Mismatches
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MEDLINE=21624277; PubWed=11752168;
Afonso C.L., Tulman B.R., Lu Z., Zsak L., Osorio F.A., Balinsky C.,
Kutish G.F., Rock D.L.;
"The genome of swinepox virus.";
J. Virol. 76:783-790(2002).
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Afonso C.L., Tulman B.R., Lu Z., Balinsky C., Osorio F.A., Zsak L.,
Kutish G.F., Rock D.L.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF410153; ALG-69867.1;
InterPro; IPR0002225; 3Bera HSD.
InterPro; IPR000977; DNA_IIgase.
PROSITE; PS00697; DNA_IIGASE_A1; UNKNOWN 1.
SEQUENCE 344 AA; 39142 MW; ECD2B807EFDE018 CRC64;
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100.0%; Score 23; DB 2; Length 344;
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1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
SPV128 hydroxysteroid dehydrogenase-like protein.
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Scoring table:

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score greater than or equal to the score of the result bein
and is derived by analysis of the total score distribution.
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             GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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                                Fibronectin protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vascular cell adhesion molecule-1 (VCAM-1) is protein found on the surface of endothelial cells that line the interior wall of capillaries. VCAM-1 recognises and binds to the integrin alpha-4beta-1 (IAHB1, or VLA-4 for very late antigen-4), a heterodimeric protein present on the surface of certain white blood cells. Binding of IAHB1 to VCAM-1 allows white blood cells to adhere to the capillary wall in areas where the tissue surrounding the capillary has been infected or damaged. Sometimes this white blood cell migration can become uncontrolled, with white blood cells flooding to the scene, causing widespread tissue damage. Cpds. capable of blocking this process may be beneficial as therapeutic
                                                                                         Human fibronectin
                                                                                                    Lamimin related
                                                                                                                                                               CS1 sequence of
                                                                                                                                                                                                                                                                                                                             VCAM-1; vascular cell adhesion molecule-1; VLA-4; very late antigen-4; inhibitor; binding; white blood cell; migration; capillary wall; tissue damage; injury; fibronectin; extracellular matrix glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New peptide(s) based on the LDV domain of fibronectin - used for inhibiting binding of alpha-4, beta-1 integrin to VCAM-1, fibronectin or invasin
                                                                                                                                                                                                                                                                                                           Alpha-4Beta-1 integrin binding inhibitory peptide 16.
                                                                                                                                                                                             ALIGNMENTS
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                                                          AAY77410
AAY78584
AAE23649
AAU74672
AAU81174
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AAY32875
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                                                                                                                                                                                                                                              AAR95719 standard; peptide; 5 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TEXA-) TEXAS BIOTECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Val-NH2"
                                                                                                                                                                                                                                                                                                                                                            CS1; CS5; HI; LDV; active site.
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Modified-site
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agents. IA4B1 also recognises the extracellular matrix glycoprotein fibronectin. Three distinct IA4B1-binding sites have been identified within fibronectin. One site is found in the HeplI region and is expressed in all isoforms; two others (CS1 and CS5) are present in the alternatively spliced type III connecting segments. CS1 has the higher affinity for IA4B1 and contains the tripeptide LDV as its minimal active site. Peptides AAR95704-805 are modeled after a portion of the CS1 peptide that include the LDV domain presented in such a way by its novel flanking sequence to produce a potent inhibitor of IA4B1 binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW25187-W25192 are peptides containing an LDV sequence or equivalent. The peptides are capable of binding to cell adhesion molecules and are used in aqueous irrigation solutions for use during and after endoscopic operations. Preferred irrigation solutions are electrolyte-free and contain in microgyml to 100 mg/ml of one or more oligopeptides containing the amino acid sequences: RGD, LDV, IDA, DGEA, GPRP, VTL, YIGSR, KQAGDV and/or REDV (given in one letter amino acid code). The solutions are especially used for irrigating the bladder during and after tumour removal by transurethral resection. The peptides protect against recurrence of tumours.
                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LDV; leucine; aspartic acid; valine; cell adhesion molecule;
binding; bladder irrigation; tumour removal; endoscopic operation;
transurethral resection; cancer; neoplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Endoscopic irrigation solns. - contg. peptide(s) that bind to cell adhesion molecules
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                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LDV-peptide capable of binding cell adhesion molecules.
                                                                                                                                                                                                        100.0%; Score 23; DB 17;
Similarity 100.0%; Pred. No. 7.8e+05;
5; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 23; DB 18;
100.0%; Pred. No. 7.8e+05;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                             AAW25192 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 6; Page 8; 8pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95DE-1029909.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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Matches 5; Conserv
                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                          5 AA;
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                                                                                                                                                                                                                                                                                                   EILDV
                                                                                                                                                                                                                                                                            1 EILDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                              AAW25192;
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                                                                                                                                                                            Sequence
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                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                           Matches
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AAW25192
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Integrin-ligand, dissociator; disaggregation; platelet thrombus; stroke; fibrinogen; glycoprotein Inb-IIIa; angina; mycastial infarction; bone; osteoclast; osteoporosis; angiogenesis; cancer; diabetic retinopathy; psoriasis; tumour; atherosclerosis; inflammatory bowel disease; asthma;
                                                                                                                                                                                                                                                                                                                                                                          Disaggregating a ligand:integrin receptor complex
                                                                                                                               organ transplant rejection; arthritis; ILD
                                                   Integrin ligand dissociator (ILD) peptide.
                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 10; 39pp; English
                          16-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                            (BURN-) BURNHAM INST.
                                                                                                                                                                                                                                                                                                                                                WPI; 1999-243586/20
                                                                                                                                                                                                                                                                   03-SEP-1997;
                                                                                                                                                                                      WO9911280-A1
                                                                                                                                                                                                                                         03-SEP-1998;
                                                                                                                                                                                                               11-MAR-1999
                                                                                                                                                           Synthetic.
 AAY03855;
                                                                                                                                                                                                                                                                                                                     Hu DD,
 The present sequence is a linear stretch of amino acids (present in fibronectin) recognised by the integrin alpha4betal. Integrins are fibronectin) recognised by the integrin alpha4betal. Integrins are receptors. The penton base protein (one of the coat proteins) of adenoviruses binds to integrins. The integrins not only proteins of adenoviruses binds to the extracellular matrix molecules. The specification describes a method of introducing an adenovirus into a cell in vitro having a particular cell surface binding site. The adenovirus is contacted with a bispecific molecule comprising a component that selectively binds a binding domain of the penton base protein of the adenovirus and a second component that selectively binds the cell surface binding site. A complex of the adenovirus and the bispecific molecule is formed, and the cell is contacted with it to allow entry of the adenovirus into the cell is the methods can be used for research and the
                                                                                                                                                                                                             penton base protein; coat proteins; adenovirus; binding site; cellular adhesion; extracellular matrix molecule; binding domain; cell surface binding site; bispecific molecule; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Methods for introducing adenovirus into cells - used for genetic engineering and gene therapy
                                                                                                                                                                                                  surface receptor,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 5;
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100.0%; Pred. No. 7.8e+05;
iive 0; Mismatches 0;
                                                                                                                                                                                                 Fibrinogen, integrin, alpha-IIb-beta3, cell
                                                                                                                                                                        Peptide recognised by integrin alpha4etal.
                                                                                                                                                                                                                                                                                                                                                                                                                               McVey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 27; Column 2; 56pp; English.
                                                                                          AAW46318 standard; Protein; 5 AA
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                                                                                                                                                                                                                                                                                                                                                                          94US-0303162
                                                                                                                                             (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                               Bruder JT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          adenovirus into the vectors can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-119984/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                     (GENV-) GENVEC INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 AB;
                                                                                                                                                                                                                                                                                                                                                                            08-SEP-1994;
                                                                                                                                                                                                                                                                  Unidentified
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                                                                                                                                             08-MAY-1998
                                                                                                                                                                                                                                                                                            US5712136-A.
                                                                                                                                                                                                                                                                                                                       27-JAN-1998.
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Wickham TJ;
                         1 EILDV
                                                                                                                   AAW46318;
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                                                               RESULT 3
                                                                               AAW46318
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98WO-US18305.

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The invention relates to integrin ligand dissociators. Disaggregation of an existing platelet thrombus in a blood vessel is due to dissociation of fibrinogen from glycoprotein Inb-IIIa. This dissociation is caused by the binding of an integrin-ligand dissociator at ligand binding site I of glycoprotein IIb-IIIa. The invention provides a method of disaggregating of an existing platelet thrombus in a blood vessel, where the platelet transmission of a blood vessel, an a subject comprises administering a compound which dissociates fibrinogen bound to a first constraint of the method is used to treat humans with unstable contraints. The method is used to treat humans with unstable congine and/or caute mycoardial infarction. The methods can be used to enact de-adhesion of osteoloasts from the bone surface to halt cond to a patient with osteoporosis. The methods can also be used to reat tumours, condition associated with and/openesis, e.g. cancer, diabbtic retinopathy, psoriasis. Inflammatory conditions, e.g. arthritas, inflammatory conditions, e.g. arthritas, inflammatory conditions, e.g. arthritas, inflammatory conditions, e.g. arthritas, inflammatory conditions, e.g. arthritas, inflammatory conditions, e.g. arthritas, inflammatory conditions, e.g. arthritas, inflammatory conditions, e.g. arthritas, inflammatory conditions, e.g. arthritas, inflammatory conditions, e.g. arthritas, inflammatory conditions, e.g. arthritas, inflammatory conditions, e.g. arthritas, inflammatory conditions, e.g. arthritas, inflammatory conditions, e.g. arthritas, inflammatory conditions, e.g. arthritas, inflammatory conditions, e.g. arthritas, inflammatory conditions, e.g. arthritas, inflammatory conditions, e.g. arthritas, inflammatory conditions, e.g. arthritas, inflammatory departure from the current strategy of treatment prior to formation of percent conditions of percent constant any encourse any entered to treat the encours.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence represents an integrin ligand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dissociator (ILD) that can be used in the method of the invention
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llarity 100.0%; Pred. No. 7.8e+05;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present
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Best Local Similarity
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AC AAY8
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Gaps

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Indels

Conservative

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ò 셤 AAY03855 standard; peptide; 5 AA.

AAY03855 ID AAY0 XX RESULT 4

Chen PG;

Huyghe BG,

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The invention relates to peptidomimetic compounds (AAY77415-Y77438)

Capable of inhibiting the binding of the VLA-4 integrin (alpha-4-beta-1, CC Cap494(CD29) to the CS-1 portion (25 amino acids) of a splice variant of the extracellular matrix protein fibronectin (FW). VLA-4 is expressed on the extracellular matrix protein fibronectin (FW). VLA-4 is expressed on the extracellular matrix protein fibronectin (FW). VLA-4 is expressed on the extracellular matrix protein fibronectin (FW). VLA-4 is expressed on the maturation and trafficking. VLA-4-mediated

CC important role in the maturation and trafficking. VLA-4-mediated

CC important role in the maturation and trafficking. VLA-4-mediated

CC critical step in the inflammatory response. The peptidomimetics of the invention may be used to treat both chronic and acute immunoinflammatory condition, demyelinating diseases of the central nervous system callograft rejection. They may also be used to treat psoriasis and other skin inflammatory bowel disease, kidney inflammation and castlon at inhibition of VLA-4(CS-1 interaction either involves the use of anti-VLA-4 antibodies, which can themselves induce an immonia response on repeated administration, or the 25-mer CS-1 peptide, which is large and costly to make and is subject to rapid proteolytic degradation. The peptidomimetics of the invention are smaller in CC comparison to the CS-1 peptide and therefore lass expensive to comparison to the CS-1 peptide and therefore lass expensive to comparison to the CS-1 peptide to imminiate to immobilised CS-1 peptide for their ability to inhibit VLA-4 Jurkat cells to immobilised CS-1 peptide for lax-714.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New peptidomimetic compounds used as cell surface fibronectin expressing receptor and VLA-4 inhibitors for treating inflammatory and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LDV peptide; VLA-4 inhibitor; very late antigen; alpha-4-beta-1; CD49d/CD29; cell adhesion; arylalkyl azolylalkanoic acid derivative; arylureidoalkyl azolylalkanoic acid derivative; inflammatory disorder; autoimmune disorder; respiratory disorder; LDV motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 23; DB 21; Length 5; 100.0%; Pred. No. 7.8e+05; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                   Gaeta FCA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 2; 243pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                   Elices MJ,
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Best Local Similarity 100.
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cardiovascular disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-182213/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 AA;
                                                               WO200002903-A1
                                                                                                                                                                                                                                                                                                                        (CYTE-) CYTEL
                                                                                                                                                                                                                                                                                                                                                                                   Arrhenius TS,
                                                                                                                                                                                         15-DEC-1998;
                                                                                                                                                                                                                                                     10-JUL-1998;
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   Mammalia
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(II) induces migration and adhesion of osteoblasts and osteoclasts and (II) inhibite proteolysis (specifically by plasmin) of extracellular matrix. (I) is preferably selected from: selectin or selectin binding ragments, proteins and peptides that facilitate cell adhesion, plasminogen activator inhibitors. Protease inhibitors and metalloprotease inhibitors are claimed examines of cell adhesion peptides used in the system of the invention. The system is used to replace, remodel or correct bone defects, e.g. fractures, fissures or bone mass loss. Incorporation of (I) into the cafficld results in rapid seeding by osteoblasts and the development of an organic matrix, i.e. the preformed scaffold replaces the rate-determining step of extracellular matrix formation. The scaffold can be designed to have a predetermined resorption/degradation rate, and may include the component of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    System for reconstructing osseous tissue, useful e.g. for treating fractures, comprises scaffold containing promoter of bone formation and inhibitor of bone resorption
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                    Bone regenerative, osteopathic, osseous tissue, reconstitution, scaffold matrix; bone formation promoter, bone resorption inhibitor, cell adhesion; osteoblast, osteoclast; bone defect, fracture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   include regulatory compounds for specific cell types.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PHAR-) PHARMACAL BIOTECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fibronectin CS1-derived peptide #33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 14; Page 32; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY77442 standard; peptide; 5 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US16800
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06-JUN-2000 (first entry)
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                                                        Cell adhesion peptide #23
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                 WO200004941-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-JUL-1998;
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                                                                                                                                                                                                                                                     Synthetic
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The invention relates to a method for treating a mammal with, or at risk of developing, chronic renal failure, involving the administration of at least one integrin antagonist. The integrin antagonists that may be used in the method include antagonists of alpha-1-subunit containing integrins or antagonists of alpha-1-subunit containing integrins. In particular, the antagonists are antibodies specific for VLA-1 (very late antigen.), alpha-1-beta-1 integrin) or VLA-4 (alpha-4-beta-1 integrin) which inhibit the interaction of the integrin and tis cognate ligand (collagen IV, and laminin in the case of VLA-1, and fibronectin and VCAM-1 in the case of VLA-4). The method of the invention may be used to treat chronic renal failure, end-stage renal disease, chronic diabetic nephropathy, diabetic collagens of propertensive glomerulosclarosis, chronic glomerulonephritis, hereditary nephritis or renal dysplasia. Sequences AAB73464-AAB73466 represent fibronectin, which inhibit fibronectin-dependent call adhesion, and may therefore be used in the method of the invention.
                                                                                                                                                                                                                            Treating a mammal in, or at a risk of developing, chronic renal failure, involves administering at least one integrin antagonist to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fibronectin fragment and fibrin related peptide SEQ ID NO:1142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 23; DB 22; Length 5; larity 100.0%; Pred. No. 7.8e+05; Conservative 0; Mismatches 0; Indels
                                                              (BIOJ ) BIOGEN INC.
(UNLO ) IMPERIAL COLLEGE SCI TECHNOLOGY & MED.
                                                                                                                                                                                                                                                                                                                         Disclosure, Page 24; 62pp; English.
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99US-0153406.
99US-0159783.
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                     99US-0153826
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Best Local Similarity
Matches 5; Conserva
                                                                                                                                                                            WPI; 2001-273408/28
                                                                                                                                   Allen A, Pusey C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5 AA;
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10-SEP-1999;
15-OCT-1999;
                     14-SEP-1999;
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                                                                                                                                                                                                                                                                           mammal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acolylalkanoic acid derivatives and related compounds (1), and their sales and prodrugs. These are are integrin inhibitors, specifically of NLA-4 (very late antigen 4, also known as alpha-4-beta-1 or CD494/CD29), which mediate cell adhesion. VLA-4 is a receptor for the cytckine-inducible cell surface protein VCAM-1 (vascular cell adhesion molecule-1) and for the alternatively spliced forms of fibronectin (FN) which contain the CS-1 domain. The novel compounds inhibit cell adhesion, and consequent or associated pathogenic processes mediated by VLA-4, and may therefore be useful in the treatment and prevention of inflammatory, autoimmune, or respiratory disorders. These include asthma, arthritis, psoriasis, multiple sclerosis, transplant rejection, diabetes, and can indiane the VLA-4-binding domain of the FN CS-1 region which contain the LDV motif and are known to inhibit fibronectin-dependent
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                                                                                                                                                                                                                                                                                                                                                                    Arylalkyl and arylureidoalkyl azolylalkanoic acid derivatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to novel arylalkyl and arylureidoalkyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 23; DB 21; Length 5; 100.0%; Pred. No. 7.8e+05; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                         Duplantier AJ, Milici AJ, Chupak LS
                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 2; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB73465 standard; peptide; 5 AA.
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                                                                                                                                   99WO-IB00973.
                                                                                                                                                                                 98US-0091180
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Best Local Similarity 100.v.
S: Conservative
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                                                                                                                                                                                                                              (PFIZ ) PFIZER PROD INC.
                                                                                                                                                                                                                                                                                                                      WPI; 2000-126762/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 AA;
                                             WO200000477-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cell adhesion.
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                                                                                                                                   31-MAY-1999;
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Synthetic
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RESULT 8 AAB7346

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that mimic a transmembrane domain and cytoplasmic domain attached to
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succiningly and maleimide groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide components to form a competidase stabilised therapeutic peptide components to form a peptidase stabilised therapeutic peptides of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular upcake and interference with physiological processes. AABB90829 to AABB941 represent peptides which can be used in the
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                                                                       Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bolypeptides useful in construction of structural models for identifying therapeutic compounds, comprises series of heptad repeats
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Integrin; transmembrane protein; alpha4 integrin inhibitor; paxillin; immunosuppressive; inflammatory bowel disease; arthritis; multiple sclerosis; asthma; atherosclerosis; wound healing.
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                         Thibaudeau K;
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                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 23; DB 22; 100.0%; Pred. No. 7.8e+05;
                       Holmes DL,
                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                           exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Integrin recognition peptide sequence #3.
                                                                                                                       Disclosure; Page 569; 733pp; English.
                         Milner PG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB50876 standard; peptide; 5 AA
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                         Bridon DP, Ezrin AM,
(CONJ-) CONJUCHEM INC
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Best Local Similarity
Local 5; Conserv?
                                                 WPI; 2001-112059/12.
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                                                                                                                                                                                                                                                                                                                                                                   s AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
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The present sequence is given in a specification relating to a polypeptide comprising a series of heptad-repeats that mimic a transmembrane domain, and a selected cytoplasmic domain attached to the putpad repeats. At least a portion of the polypeptide is prepared recombinantly or at least 1 heptad repeat in the series has a different amino acid sequence to other heptad repeats in the series. The control of structural models which are useful for evaluating structure and activity of a selected occupied and clustered transmembrane protein having the selected cytoplasmic domain and for identifying therapeutic compounds. It is also useful for and for identifying therapeutic compounds. It is also useful for and for identifying the structural model with paxillin or a paxillin related molecule in the presence and absence of a test agent paxillin related molecule in the presence and absence of the test and determining binding of paxillin related molecule to the structural model. A decrease in binding in the presence of the test agent indicates that the test agent is an inhibitor of alpha4 integrin blocking immune responses in conditions such as inflammatory bowel disease, arthritis, multiple sclerosis and asthma and in inhibiting atherosclerosis and scarring during wound healing.
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inflammation; thrombosis; malignancy.
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100.0%; Pred. No. 7.8e+05;
iive 0; Mismatches 0;
                                                                            Disclosure, Page 2; 37pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide #3 recognised by integrin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB59135 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAY-2000; 2000WO-US14656.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ginsberg MH, Pfaff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 AA;
heptad repeats
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The invention relates to peptidomimetic compounds (AAY77415-Y77438) capable of inhibiting the binding of the VLA-4 integrin (alpha-4-beta-1, CD49d/CD29) to the CS-1 portion (25 amino acids) of a splice variant of the extracellular matrix protein fibronectin (FN). VLA-4 is expressed on the extracellular matrix protein fibronectin (FN). VLA-4 is expressed on important role in the maturation and trafficking. VLA-4-mediated leukocyte adhesion to the CS-1 FN/VLA-4 interaction plays an important role in the maturation and trafficking. VLA-4-mediated leukocyte adhesion to the CS-1 FN/VLA-4 interaction plays and runcortion may be used to treat both chronic and acute immunoinflammatory conditions, such as asthma, rheumatoid arthritis, osteoarthritis and allograft rejection. They may also be used to treat psoriasis and other skin inflammations, demyelinating diseases of the central nervous system (e.g., multiple sclerosis), allergies, atherosclerosis, colitis, cliabetes, inflammatory bowel disease, kidney inflammation and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fibronectin, FN: CS-1; endothelial cell; VLA-4 integrin; alpha-4-beta-1; CD49d/CD29; leukocyte; inflammatory cell; inflammation; cell adhesion; inhibitor; peptidomimetic; autoimmune disease; inflammatory disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New peptidomimetic compounds used as cell surface fibronectin expressing receptor and VLA-4 inhibitors for treating inflammatory and cardiovascular disorders
                                                                                                                                                                                                                                                                                                               Gaps
The present invention relates to a peptide with a series of heptad-repeats that mimic a transmembrane domain and a selected cytoplasmic domain attached to the heptad respeats. The invention is useful for evaluating structure and activity of a selected occupied and clustered transmembrane protein with the selected cytoplasmic domain and for identifying therapeutic compounds. It is also useful for identifying a cytoplasmic domain binding partner. It is may be used to study protein interactions with transmembrane proteins such as integrin, which can be used to treat conditions in which over activity of integrins is involved, such as inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen PG;
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                                                                                                                                                                                                                                                                         Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Huyghe BG,
                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                         100.0%; Score 23; DB 22; 100.0%; Pred. No. 7.8e+05;
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                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaeta FCA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fibronectin CS1-derived peptide #34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 2; 243pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY77443 standard; peptide; 6 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arrhenius TS, Elices MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                             thrombosis and malignancy
                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
5; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-182213/16.
                                                                                                                                                                                                                                     5 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-MAY-2000
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                                                                                                                                                                                                                                     Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY77443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia.
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The invention relates to peptidomimetic compounds (AAY77415-Y77438) capable of inhibiting the binding of the VLA-4 integrin (alpha-4-beta-1, CD49d/CD29) to the CS-1 portion (25 amino acids) of a splice variant of the extracellular matrix protein fibronectin (FW). VLA-4 is expressed on the surface of leukocytes; the CS-1 FW/VLA-4 interaction plays an important role in the maturation and trafficking. VLA-4-mediated important role in the maturation and trafficking. VLA-4-mediated clucyte adhesion to the CS-1 FW/VLA-4 interaction plays an elukocyte adhesion to the CS-1 FW of endothelial cells is also a critical step in the inflammatory response. The peptidomimetics of the cinvention may be used to treat both chronic and acute immunoinflammatory conditions, such as asthma, rheumatoid arthritis, osteoarthritis and allograft rejection. They may also be used to treat pooriasis and other skin inflammations, demyelinating diseases of the central nervous system (e.g., multiple sclerosis), allergies, atherosclerosis, colitis, diabetes, inflammatory bowel disease, kidney inflammation and creation either
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restenosis. Prior art inhibition of VLA-4/CS-1 interaction either involves the use of anti-VLA-4 antibodies, which can themselves induce an immune response on repeated administration, or the 25-mer CS-1 peptide, which is large and costly to make and is subject to rapid proteolytic degradation. The peptidomimetics of the invention are smaller in comparison to the CS-1 peptide and therefore less expensive to manufacture, and are resistant to proteolysis. Sequences AAY77411-Y77414 and AAY77434-Y77444 represent fragments of the CS-1 peptide tested for their ability to inhibit VLA-4 Jurkat cells to immobilised CS-1 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fibronectin; FN; CS-1; endothelial cell; VLA-4 integrin; alpha-4-beta-1; CD49d/CD29; leukocyte; inflammatory cell; inflammation; cell adhesion; inhibitor; peptidomimetic; autoimmune disease; inflammatory disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New peptidomimetic compounds used as cell surface fibronectin expressing receptor and VLA-4 inhibitors for treating inflammatory and cardiovascular disorders
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen PG;
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                                                                                                                                                                                                                                                                        100.0%; Score 23; DB 21; Length 6; 100.0%; Pred. No. 7.8e+05; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         He Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaeta FCA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fibronectin CS1-derived peptide #35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Fig 2; 243pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY77444 standard; peptide; 6 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arrhenius TS, Elices MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                         Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-182213/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CYTE-) CYTEL CORP.
                                                                                                                                                                                                                                      6 AA;
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                                                                                                                                                                                                                                                                                                                                                            1 EILDV 5
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                                                                                                                                                                                                                                                                                                                                                                                        2 EILDV
                                                                                                                                                                                           (AAY77410)
                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY77444;
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Gaps

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Indels

Length

Score 23; DB 19; Pred. No. 7.8e+05; 0; Mismatches

100.0%;

Conservative

Query Match Best Local Similarity Matches 5; Conserv

1 EILDV

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involves the use of anti-VLA-4 antibodies, which can themselves induce ar immune response on repeated administration, or the 25-mer CS-1 peptide, which is large and costly to make and is subject to rapid proteolytic degradation. The peptidomimetics of the invention are smaller in comparison to the CS-1 peptide and therefore less expensive to an anulacture, and are resistant to proteolysis. Sequences AAY77411-Y77414 and AX77434-X77444 represent fragments of the CS-1 peptide tested for their ability to inhibit VLA-4 Jurkat cells to immobilised CS-1 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents an alpha4 integrins targeting sequence, which is used in an example from the present invention. The present invention describes a chimeric adenovirus fibre protein (AFP) containing a constrained non-native amino acid sequence. The non-native amino acid sequence allows the chimeric fibre (or a vector comprising the chimeric fibre) to more efficiently bind to and enter cells. The products can be used for gene therapy, for treating cancer, e.g. melanoma, glioma and lung cancers as well as genetic disorders, e.g. vestic fibrosis, haemophilia and muscular dystrophy as well as pathogenic infections, e.g. HIV, tuberculosis and hepatitis and also for heart disease, to e.g. prevent restenosis following angioplasty or to promote angiogenesis to reperfuse necrotic tissue, and in autoimmune disorders, e.g. Crohn's disease, colitis, rheumatoid arthritis, and Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric; adenovirus; fiber protein; binding; targeting; coat protein; constrained peptide motif; gene therapy; cancer; heart disease; autoimmune disorder.
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric adenovirus fibre proteins - containing non-native amino acid sequence to provide for binding and entry into cells, especially for gene therapy
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                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                 100.0%; Score 23; DB 21;
100.0%; Pred. No. 7.8e+05;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alpha4 integrins targeting sequence SEQ ID NO:80.
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                                                                                                                                                                                                                                                                                                                                                                                                                 AAW56065 standard; peptide; 7 AA
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                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kovesdi I, Roelvink PW,
                                                                                                                                                                                                  WPI; 1998-169169/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENV-) GENVEC INC.
                                                                                                                                                                                 6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mastadenovirus.
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                                                                                                                                                (AAY77410).
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                                                                                                                                                                                   Sequence
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Fibronectin, extracellular matrix receptor; ECMR: type III; connecting segment; IIICS; adhesion; alpha4beta1; lymphocyte; autoimmune disease; allergy; asthma; ligand.

89US-0402389. 90WO-US04978.

31-AUG-1990; 01-SEP-1989;

WO9103252-A 21-MAR-1991

Synthetic.

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(WAYN/) WAYNER

Wayner E;

Peptide #352 derived from Cs-1 peptide of IIICS region.

(first entry)

04-JUN-1991

AAR11361;

AAR11361 standard; peptide; 8 AA.

RESULT 15

AAR11361

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                                                                                                                                                                                                                                                                                                                                                 Inhibition of lymphocyte adherence to vascular endothelium - using a novel antibody or peptide for treatment of auto-immune disease, asthma, allergy etc.
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llarity 100.0%; Pred. No. 7.8e+05;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                     Claim 10; Page 74; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR28885 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                          WPI; 1991-101865/14.
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les 5; Conserv
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Matches
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ID AAR2
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Sequence

us-09-251-073a-16.open.rag

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92JP-0271293
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                                                                                                                                                                        WPI; 1994-173758/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 AA;
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   JP06116288-A.
                                                                                                     09-OCT-1992;
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11-JUL-1994;
                                                                    09-OCT-1992;
                                    26-APR-1994.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequences given in AAR28885-86 are peptides which have been shown to inhibit cell adhesion. These peptides can be used as the active component in a cancer metastasis inhibitor, a wound healer, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunosuppressant, a platelet aggregation inhibitor or a neuropathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "N-terminal is attached to propenamide po"
                                                                                                     Cell adhesion; cancer; metastasis inhibitor; wound healer; nmmunosuppressant; platelet; aggregation inhibitor; neuropathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Propenamide; cell adhesion antagonist; anticancer; antitumour; lymphocyte activation; metastasis; cell culture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide deriv. - useful as cancer metastasis inhibitor, wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 23; DB 13; Length 8; 100.0%; Pred. No. 7.8e+05;
                                                                                                                                                                                                                          "Terminal Glu residue is linked to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polymer-bound cell surface receptor binding peptide
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                                                                                                                                                                                                                                                                                               present in the mo
optically active
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                                                                                                                                                                                            Location/Qualifiers
                                                                  Cell adhesion inhibitory peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR44360 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 2; 10pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                healer, immunosuppressant, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (FUJF ) FUJI PHOTO FILM CO LID
                                                                                                                                                                                                                                                                                                                                                                                                                      91JP-0062146
                                                                                                                                                                                                                                                                                                                                                                                                                                                         91JP-0062146
                                  (first entry)
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nes 5; Conservative
                                                                                                                                                                                                                              /note=
                                                                                                     Cell adhesion; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1992-395376/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 AA;
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Modified-site
                                                                                                                                                                                            Key
Modified-site
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                                                                                                                                                                                                                                                                                                                                                    JP04295497-A
                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAR-1991;
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                                  23-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                    20-0CT-1992
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                                                                                                                                                       Synthetic.
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AAR28885;
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VLA-4; inhibitor; binding peptide; leucocyte adhesion; CD49d/CD29; CDR; alpha4beta1 integrin; VCAM-1; endothelial cell; antibody; meningitis; complementarity determining region; inflammatory brain disorder; therapy; multiple aclerosis; encephalitis; Alzheimar's disease; atherosclerosis; AlDS dementia; diabetes; inflammatory bowel disease; tumour metastasses; rheumatoid arthritis; transplant rejection; myocardial ischaemla; asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to new propenamide compounds of formula RIR2C=C(R3)CO-(NH)x-A and their (optionally crosslinked) polymers, where R1 and R2 are H or COOH, R3 = H, Me, Et, halo or carboxymethyl, A is a peptide of formula -(R4)x-(CO)x-(G1U)x-(IL8)x-Leu-App-Val-(Pro)x-(Ser)x-(Thr)Xin-(Z)x-(R5)x-, where Z = 0 or NH, one of R4 and R5 is a terminal H and the other is absent or 1-11C alkylene or 6-11C arylene each of which may be optionally substituted, n = 1 - 5, and x = 0 or 1. The compounds and their polymers combine with cell surface receptors and prevent cell adhesion. They can be used to inhibit cancer metastasis and to activate lymphocytes, and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                    New propenamide cpds. which are N-substd. by specified peptide, and new polymers - are cell adhesion inhibitors useful e.g. for preventing cancer metastasis
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Pred. No. 7.8e+05;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  components of cell culture substrates.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR92536 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 2; 8pp; Japanese.
                                                                      (FUJF ) FUJI PHOTO FILM CO LTD
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92JP-0271293.
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94US-0273055.
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AAW25187-W25192 are peptides containing an LDV sequence or equivalent. The peptides are capable of binding to cell adhesion molecules and are used in aqueous irrigation solutions for use during and after endoscopic operations. Preferred irrigation solutions are electrolyte-free and contain 1 microg/ml to 100 mg/ml of one or more oligopeptides containing the amino acid sequences: RGD, LDV, IDA, DGEA, GPRP, VTL, YIGSR, KQAGDV and/or REDV (given in one letter amino acid acide). The solutions are especially used for irrigating the bladder during and after tumour removal by transurethral resection. The peptides protect against recurrence of tumours.
                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptides AAW63133-34 appear in the specification, which describes non-viral mediated methods for incorporating a macromolecule into a cell. The methods and products permit the immobilisation, microinjection and recovery of cells. The methods can be used for introducing genetic material, proteins, peptides and immunoglobulins into living cells. In partial, they can be used in gene therapy for the treatment of disorders such as thalassemia and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Non-viral; immobilisation; microinjection; gene therapy; treatment;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Non-viral incorporation of molecules into cells - by treal surface with adhesive molecule, contacting with cells and introducing molecules by, e.g. micro:injection
                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                  100.0%; Score 23; DB 18; 100.0%; Pred. No. 7.8e+05;
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llarity 100.0%; Pred. No. 7.8e+05;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide sequence of the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 71; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW63133 standard; peptide; 8 AA.
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                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thallasemia; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-377639/32.
                                                                                                                                                                                                                                                                         Local Similarity
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                8 A.A.;
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                                                                                                                                                                                                                                                                                                                             1 EILDV 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
                                                                                                                                                                                                                                                                                         5;
                                                                                                                                                                                                                                                                                                                                                        1 EILDV
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                                                                                                                                                                                                    AAR92536-R92555 represents VLA-4 binding peptides derived from the antibody 21/6. VLA-4 is also known as alpha4betal integrin and catiody 21/6. VLA-4 binds to the non-matrix molecule VCAM-1, which is expressed by which is also known as alpha4betal integrin and expressed by endothelial and other cells. These sequences mimic a short consensus sequence in the heavy chain complementarity determining region (CDR) 3 of monoclonal antibodies against alpha4betal integrin. These sequences inhibit the adhesion of leucocytes mediated by VLA-4. It is useful for treating inflammatory brain disorders (especially multiple sclerosis), meningitis, encephalitis, asthma, Alzheimer's disease, rheumatoid arthritis, transplant rejection, tumour metastsass and myocardial ischaemia. These sequences can also be labelled, and can then myocardial ischaemia. These sequences can also be labelled, and can then the used for in vivo or in vitro diagnosis, such as monitoring inflammatory responses, isolating elecocytes, in assasys for inhibitors of VLA-4/VCAM-1 interactions and imaging sites of inflammation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                New peptide(s) that bind VLA-4, inhibit leucocyte adhesion - useful esp. for treatment of inflammatory disease, e.g. multiple sclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LDV; leucine; aspartic acid; valine; cell adhesion molecule; binding; bladder irrigation; tumour removal; endoscopic operation; transurethral resection; cancer; neoplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contg. peptide(s) that bind to cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LDV-peptide capable of binding cell adhesion molecules.
                                         Yednock TA;
                                                                                                                                                                       Example 7; Page 26; 42pp; English.
 (ATHE-) ATHENA NEUROSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW25190 standard; peptide; 8 AA.
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Matches 5; Conservative
                                   Pleiss MA, Thorsett ED,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (FREP ) FRESENIUS AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW25190;
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98US-0025622.
                                                                                                                                                                                 Gailit J,
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                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                 8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-FEB-1998;
                                                                               WO9942126-A1.
                                                                                                                      10-FEB-1999;
                                                                                                                                          18-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-FEB-1999;
                                                           Homo sapiens
                                                                                                  26-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EILDV
                                                                                                                                                                                 Clark RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY32874;
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                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a specifically claimed non-native amino acid sequence from a chimeric adenovirus fibre protein (AFP) of the present invention. The non-native amino acid sequence allows the chimeric fibre (or a vector comprising the chimeric fibre) to more efficiently bind to and enter cells. The products can be used for gene farrangy. For trearing cancer, e.g. melanoma, glioma and lung cancers as well as genetic disorders, e.g. cystic fibrosis, haemophilia and muscular dystrophy as well as pathogenic infections, e.g. HIV, truberculosis and hepatitis and also for heart disease, to e.g. prevent restenosis following angioplasty or to promote angiogenesis to reperfuse necrotic tissue, and in autoimmune disorders, e.g. Crohn's disease, colitis, rheumatoid arthritis, and Alzheimer's disease.
                                                                                                                             Chimeric; adenovirus; fiber protein; binding; targeting; coat protein; constrained peptide motif; gene therapy; cancer; heart disease; autoimmune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                             Chimeric adenovirus fiber protein non-native amino acid sequence 56
                                                                                                                                                                                                                                                                                                                                                 Chimeric adenovirus fibre proteins - containing non-native amino acid sequence to provide for binding and entry into cells, especially for gene therapy
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100.0%; Pred. No. 7.8e+05;
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                                                                                                                                                                                                                                                                                                          Wickham TJ;
                                                                                                                                                                                                                                                                                                                                                                                        Claim 7; Page 84; 124pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY32862 standard; peptide; 8 AA
                                                 AAW56046 standard; peptide; 8 AA.
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Best Local Similarity 100.v.
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                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                          Kovesdi I, Roelvink PW,
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                                                                                                                                                                                                                                                                                     (GENV-) GENVEC INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 AA;
                                                                                                                                                                                  Mastadenovirus.
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                                                                                                                                                                                                                                             21-AUG-1997;
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 1 EILDV
                                                                                                                                                                        Synthetic.
                                                                    AAW56046;
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                             RESULT 21
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Fibronectin, extracellular matrix; wound healing promoter; IIICS domain; cell binding domain; heparin II binding domain; haemostasis; therapy; surgical incisional wound; traumatic wound; radiation wound; cancer extirpation; venous leg ulcer; diabetic ulcer; pressure ulcer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fibronectin; extracellular matrix. open wound healing; IIICS domain; acute gaping cutaneous wound; chronic cutaneous ulcer; therapy; wound healing promoter; cell binding domain; heparin II binding domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Extracellular matrix for promoting wound healing containing recombinant fibronectin-derived peptide and backbone matrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 23; DB 20; Length 8; larity 100.0%; Pred. No. 7.8e+05; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Greiling D;
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(UYNC-) UNIV NORTH CAROLINA.
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                         Boucher RC,
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EILDV
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                                                                                                                                                  This sequence represents a fibronectin protein fragment used in the extracellular matrix of the invention. The extracellular matrix comprises two or more fibronectin domains in a backbone matrix, and is used to enhance wound healing. The fibronectin domain peptides used are preferably from the IIICS domain, the cell binding domain, or the heparin II binding domain of human fibronectin. The matrix facilitates wound healing by providing an environment that intrinsically recruits new tissue cells to the wound site. The new matrix is useful for facilitating wound healing, especially useful for treating open wounds such as acute gaping cutaneous wounds and chronic cutaneous ulcers. The problem of chronic, non-healing wounds is severe. These open wounds require long-term care and procedures that are costly and labour intensive.

The prior compositions and matrices have not been useful or cost effective. The present invention provides a matrix for wound healing that meets these requirements, and overcomes the deficiencies of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pharmaceutical composition; gene therapy; junctional complex disruption; cytostatic; cardiant; vasotropic; antiinflammatory; antilipaemic; cytostatic fibrosis; inflammatory disease; fibrotic lung disease; peripheral vascular disease; coronary arterial disease; restenosis; hypercholesterolaemia; cancer; human; vitronectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                       New extracellular matrix used to accelerate healing of acute gaping cutaneous wounds and chronic cutaneous ulcers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vitronectin peptide used to enhance viral vector binding affinity.
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          (UYNY ) UNIV NEW YORK STATE RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB35734 standard; peptide; 8 AA.
                                                                                                                             Claim 5; Page 19; 43pp; English
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99GB-0009073.
99GB-0009297.
99US-0153757.
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Best Local Similarity
5; Conserve
                                                              WPI; 1999-527415/44
                                                                                                                                                                                                                                                                                                                                                                                              8 AA;
                                                                                                                                                                                                                                                                                                                                                                       prior matrices
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20-APR-1999;
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13-SEP-1999
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                                    Clark RA,
                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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This invention relates to a pharmaceutical composition used for gene therapy, comprising a nucleic acid encoding a therapeutic gene and a promoter, a transfection vehicle and an agent to disrupt the function of the junctional complex in the cells. The pharmaceutical composition of cytostatic, cardiant, vasotropic, antiinflammatory and antilipaemic activity. The pharmaceutical composition is useful for gene therapy and for enhancing efficiency of gene delivery to cells. The composition is useful for gene therapy of cytic fibrosis, inflammatory or fibrotic lung diseases, peripheral vascular disease, coronary arterial diseases, restensis, hypercholesterolaemia and cancer. The present sequence represents a vitronectin peptide. The peptide can be used to enhance the binding affinity of a viral vector used in the pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        System for reconstructing osseous tissue, useful e.g. for treating fractures, comprises scaffold containing promoter of bone formation and
                                                                                                          nucleic acid encoding therapeutic gene and a promoter, transfection vehicle and an agent which disrupts function of junctional complex in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bone regenerative; osteopathic; osseous tissue; reconstitution; scaffold matrix; bone formation promoter; bone resorption inhibitor; cell adhesion; osteoblast; osteoclast; bone defect; fracture.
                                                                                 Novel pharmaceutical composition useful for gene therapy, comprises
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Pred. No. 7.8e+05;
Man Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                            Disclosure; Page 12; 51pp; English.
Johnson LG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY80489 standard; peptide; 8 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        composition of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inhibitor of bone resorption
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Best Local Similarity 100.vv
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Ford MJ,
                                      WPI; 2000-679557/66.
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bone formation and a component that decreases bone resorption (II).

Li inhibite sugration and adhesion of osteoblasts and osteoclasts and (II) inhibites proteolysis (specifically by plasmin) of extracellular matrix. (I) is preferably selected from: selectin or selectin binding fragments, proteins and peptides that facilitate cell adhesion, plasminogen activator inhibitors, protease inhibitors and metalloprocease inhibitors. Pre peptides AAY8046-Y80492 are claimed metalloprocease inhibitors peptides used in the system of the invention. The system is used to replace, remodel or correct bone defects, e.g. fractures, fissures or bone mass loss: Incorporation of (I) into the scaffold results in rapid seeding by osteoblasts and the development of an organic matrix, i.e. the preformed scaffold replaces the rate-determining step of extracellular matrix formation. The scaffold can be designed to have a predetermined resorption/degradation rate, and may
                      ention relates to a novel system for reconstitution of ossecomprising a scaffold carrying a compound (1) that promotes
                                                                                                                                                                                                                                                                                                                                                                                                          include regulatory compounds for specific cell types.
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nes 5; Conserv
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Gaps

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100.0%; Score 23; DB 21; Length 8; 100.0%; Pred. No. 7.8e+05; Live 0; Mismatches 0; Indels

AAY69618 standard; peptide; 8 AA. VLA-4 inhibitor peptide #1. (first entry)

LDV peptide; VLA-4 inhibitor; very late antigen; alpha-4-beta-1; CD49d/CD29; cell adhesion; arylalkyl azolylalkanoic acid derivative; arylureidoalkyl azolylalkanoic acid derivative; inflammatory disorder; autoimmune disorder; respiratory disorder; LDV motif.

Synthetic.

WO200000477-A1 06-JAN-2000. 31-MAY-1999;

98US-0091180

30-JUN-1998;

(PFIZ) PFIZER PROD INC.

Chupak LS;

Milici AJ,

Duplantier AJ,

WPI; 2000-126762/11.

Arylalkyl and arylureidoalkyl azolylalkanoic acid derivatives

Disclosure; Page 2; 120pp; English.

The invention relates to novel arylalkyl and arylureidoalkyl azolylalkanoic acid derivatives and related compounds (I), and their salts and prodrugs. These are are integrin inhibitors, specifically of VLA-4 (very late antigen 4, also known as alpha-4-beta-1 or CD49d/CD29), which mediate cell adhesion. VLA-4 is a receptor for the cytokinemidicable cell aurface protein VCA+1 is a veceptor for the cytokinemolecule-1) and for the alternatively spliced forms of fibronectin (FN) which contain the CS-1 domain. The novel compounds inhibit cell adhesion,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a method for treating a mammal with, or at risk of developing, chronic renal failure, involving the administration of at least one integrin antagonist. The integrin antagonists that may be used in the method include antagonists of alpha-4-subunit containing integrins or antagonists are antibodies specific for VLA-1 (very late antigon-1, alpha-1-beta-1 integrin) or VLA-4 (alpha-4-beta-1 integrin) which inhibit the interaction of the integrin and its cognate ligand (collagen I, collagen IV, and lamini in the case of VLA-1, and fibronectin and VCAM-1 in the case of VLA-4). The method of the invention may be used to treat chronic renal failure, end-stage renal disease, chronic diabetic nephropathy, diabetic
and consequent or associated pathogenic processes mediated by VLA-4, and way therefore be useful in the treatment and prevention of inflammatory, autoimmune, or respiratory decoders. These include asthma, arthritis, psoriasis, multiple sclerosis, transplant rejection, diabetes, and inflammatory bowel disease. Sequences APK5918-Y5520 respresent poptides derived from the VLA-4-binding domain of the FN CS-1 region which contain the LDV motif and are known to inhibit fibronectin-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Treating a mammal in, or at a risk of developing, chronic renal failure, involves administering at least one integrin antagonist to the
                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Integrin antagonist; VLA-4 antagonist; alpha-4-beta-1 integrin; very late antigen; antibody; kidney disease; chronic renal fallure; end-stage renal disease; chronic diabetic nephropathy; diabetic chronic glomerulopathy; diabetic renal hypertrophy; hypertensive aphroscalerosis; hypertensive dlomeruloscalerosis; chronic glomerulonephritis; hereditary nephritis; renal dysplasis; nephrotropic; cell adhesion inhibition; fibronectin CS-1 region.
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                                                                                                                                                                                                 Length 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fibronectin VLA-4 binding domain-derived octapeptide.
                                                                                                                                                                                                 Score 23; DB 21;
Pred. No. 7.8e+05;
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                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                  AAB73464 standard; peptide; 8 AA.
                                                                                                                                                                                                  100.0%;
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                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BIOJ ) BIOGEN INC
                                                                                                                                                               8 AA;
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                                                                                                                                cell adhesion.
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                                                                                                                                                                                                                                                                         EILDV
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                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                              RESULT 27
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exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attended to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides of 3-50 amino acids. (I) are useful for modifying therapeutic peptides of 3-50 amino acids. (I) are useful for modifying therapeutic peptides of the peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular upcake and interference with physiological processes. AAB90829 to AAB92441 represent peptides which can be used in the
                                                                                                                                                        o;
glomerulopathy, diabetic renal hypertrophy, hypertensive nephrosclerosis, hypertensive glomerulosclerosis, chronic glomerulonephritis, hereditary nephritis or renal dysplasia. Sequences AAB73464-AAB73466 represent peptides derived from the VLA-4 binding domain (CS-1 region) of fibronectin, which inhibit fibronectin-dependent cell adhesion, and may therefore be used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                             Protection, endogenous therapeutic peptide; peptidase, conjugation, blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
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                                                                                                                                                                                                                                                                                                                                                                 Fibronectin fragment and fibrin related peptide SEQ ID NO:1143.
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                                                                                                                           100.0%; Score 23; DB 22; Length 8; 100.0%; Pred. No. 7.8e+05; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Page 569; 733pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bridon DP, Ezrin AM, Milner PG,
                                                                                                                                                                                                                                                                                  AAB91967 standard; Peptide; 8 AA.
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99US-0153406.
99US-0159783.
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                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                        Conservative
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                                                                                                           Query Match
Best Local Similarity
Local 5; Conserve
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                                                                                                  8 AA;
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10-SEP-1999;
15-OCT-1999;
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                                                                                                  Sequence
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                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New peptide(s) contg. PEG derivs. - are cell adhesion and platelet adhesion inhibitors, useful as carcinoma metastasis inhibitors, immuno-regulators and for wound healing
                                      Length 8;
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                                      Score 23; DB 22;
Pred. No. 7.8e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Triazine; polyethylene glycol; agglutination.
                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                             Adhesion inhibitor peptide #1
                                    100.0%;
ilarity 100.0%;
Conservative 0
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Best Local Similarity 100.00
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                 Query Match
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8 AA;
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The invention relates to peptidomimetic compounds (AAY77415-Y77438) capable of inhibiting the binding of the VLA-4 integrin (alpha-4-beta-1, CD494/CD99) to the CS-1 portion (55 amino acids) of a splice variant of the extracellular matrix protein fibronectin (FN). VLA-4 is expressed on the surface of leukocytes; the CS-1 FN/VLA-4 interaction plays an important role in the maturation and trafficking. VLA-4-mediated leukocyte adhesion to the CS-1 FN of endothelial cells is also a critical step in the inflammatory response. The peptidomimetics of the invention may be used to treat both chronic and acute immunoinflammatory conditions, such as sathma, rheumatoid arthritis is osteoarthritis and allograft rejection. They may also be used to treat pooriaals and other skin inflammations, demyelinating diseases of the central nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fibronectin, FN; CS-1; endothelial cell; VLA-4 integrin; alpha-4-beta-1; CD49d/CD29; leukocyte; inflammatory cell; inflammation; cell adhesion; inhibitor; peptidomimetic; autoimmune disease; inflammatory disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New peptidomimetic compounds used as cell surface fibronectin expressing receptor and VLA-4 inhibitors for treating inflammatory and cardiovascular disorders
                                                                                                                                                The sequences given in AAR28885-86 are peptides which have been shown to inhibit cell adhesion. These peptides can be used as the active component in a cancer metaeris inhibitor, a wound healer, an immunosuppressant, a platelet aggregation inhibitor or a neuropathy
                                                    Peptide deriv. - useful as cancer metastasis inhibitor, wound healer, immunosuppressant, etc.
                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                100.0%; Score 23; DB 13;
100.0%; Pred. No. 7.8e+05;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY77436 standard; peptide; 9 AA.
                                                                                                               Claim 1; Page 2; 10pp; Japanese
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Matches 5; Conserv
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                                                                                                                                                                                                                                                             9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents an animal cell adhesion peptide. It is useful as an animal cell adhesion inhibitor or platelet aggregation/adhesion inhibitor.
                                                                                                                                                                                                                                                                                                                                                      New polypepitide(s) contg. repeat units of octa:peptide(s) - for inhibiting adhesion of cells (e.g. to fibronectin) and aggregation adhesion of platelets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell adhesion; cancer; metastasis inhibitor; wound healer; lmmunosuppressant; platelet; aggregation inhibitor; neuropathy.
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                                   platelet aggregation inhibitor; platelet adhesion inhibitor;
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100.0%; Pred. No. 7.8e+05;
iive 0; Mismatches 0;
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Cell adhesion inhibitor #2.
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Modified-Bite
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                                                        fibronectin
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(e.g., multiple sclerosis), allergies, atherosclerosis, colitis, diabetes, inflammatory bowel dieease, kidney inflammation and restenosis. Prior art inhibition of VLA-4CS-1 interaction either involves the use of anti-VTA-4 antibodies, which can themselves induce an immune response on repeated administration, or the 25-mer CS-1 peptide, which is large and costly to make and is subject to rapid proteolytic degradation. The peptidemineties of the invention are smaller in comparison to the CS-1 peptide and therefore less expensive to and are resistent to proteolysis. Sequences AA77141-Y77414 and AA77444 represent fragments of the CS-1 peptide tested for their ability to inhibit VLA-4 Jurkat cells to immobilised CS-1 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to peptidomimetic compounds (AAY77415-Y77438) capable of inhibiting the binding of the VLA-4 integrin (alpha-4-beta-1, CD494/CD29) to the CS-1 portion (25 amino acids) of a splice variant of the extracellular matrix protein fibromectin (FN) vLA-4 is expressed on the surface of leukocytes; the CS-1 FN/VLA-4 interaction plays an important role in the maturation and trafficking vLA-4-mediated leukocyte adhesion to the CS-1 FN of endothelial cells is also a critical step in the inflammatory response. The peptidomimetics of the invention may be used to treat both chronic and acute immunoinflammatory conditions, such as asthma, rheumatoid arthritis, osteoarthritis and allograft rejection. They may also be used to treat psoriasis and other skin inflammations, demyeliating diseases of the central nervous system (e.g., multiple sclerosis), allergies, atherosclerosis, colitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fibronectin, FN; CS-1; endothelial cell; VLA-4 integrin; alpha-4-beta-1; CD49d/CD29; leukocyte; inflammatory cell; inflammation; cell adhesion; inhibitor; peptidomimetic; autoimmune disease; inflammatory disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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ive 0; Mismatches 0; Indels
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diabetes, inflammatory bowel disease, kidney inflammation and restenosis. Prior art inhibition of VLA-4/CS-1 interaction either involves the use of anti-VLA-4 antibodies, which can themselves induce an immune response on repeated administration, or the 25-mer CS-1 peptide, which is large and costly to make and is subject to rapid proteolytic degradation. The peptidomimetics of the invention are smaller in comparison to the CS-1 peptide and therefore less expensive to manufacture, and are resistant to proteolysis. Sequences AAY7411-Y77414 and AAY77434-Y77444 represent fragments of the CS-1 peptide tested for their ability to inhibit VLA-4 Jurkat cells to immobilised CS-1 peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fibronectin, FN; CS-1; endothelial cell; VLA-4 integrin; alpha-4-beta-1; CD49d/CD29; leukocyte; inflammatory cell; inflammation; cell adhesion; inhibitor; peptidomimetic; autoimmune disease; inflammatory disorder.
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involves the use of anti-VLA-4 antibodies, which can themselves induce an immune response on repeated administration, or the 25-mer CS-1 peptide, which is large and costly to make and is subject to rapid proteolytic degradation. The peptidomimetics of the invention are smaller in comparison to the CS-1 peptide and therefore less expensive to manufacture, and are resistent to proteolytis. Sequences AAY7141-Y77414 and AAY77434-Y77444 represent fragments of the CS-1 peptide tested for their ability to inhibit VIA-4 Jurkat cells to immobilised CS-1 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a 2,4,6-trisubstituted s-triazine ring, where one substitution is a polyethylene glycol chain [CH3 (CH2CH2)] no-6 "no 1-150)] and the cher is either another, same, polyethylene glycol chain, or another, same, peptide chain. For examples see also AAR29631-32. These PEG derivates or their salts are useful as animal cell adhesion inhibitors, or as platelet agglutination or adhesion inhibitors. They may also be used as carcinoma metastasis inhibitors, wound healing drugs and
                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               One of 1 or 2 of these chains are attached via the N- or C-terminal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New peptide(s) contg. PEG derivs. - are cell adhesion and platelet adhesion inhibitors, useful as carcinoma metastasis inhibitors, immuno-regulators and for wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 23; DB 13; Length 10;
Pred. No. 31;
                                                                                                                                                                                                   Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or may be absent"
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Similarity 100.0%; Pred. No. 7.8e+05;
5; Conservative 0; Mismatches 0:
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                                                                                                                                                                                                                                                                                                                                                                                  AAR25998 standard; peptide; 10 AA.
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Matches 5; Conserv
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                                                                                                                                                                   9 AA;
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"Any amino acid or absent may also have opt. -O- or -NH- followed by an opt substd. (un) satd. 8-24 C alkyl."

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/note= "Any amino acid or absent
may also have opt -CO- followed by an opt.
substd. (un) satd. 8-24 C alkyl."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide deriv., for cancer metastasis inhibitor - useful as wound
healer, immune- and platelet aggregation inhibitor and neuropathy
 wound healing; immune inhibitor; neuropathy drug.
                                                                     Location/Qualifiers
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/note= '
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                                                                                       Misc-difference
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Misc-difference
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                              note= "May be an amino acid, peptide or absent."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "May be an amino acid, peptide or absent."
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                                                                                                                                                                                                                                                                                                       platelet aggregation inhibitor; platelet adhesion inhibitor; fibronectin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 23; DB 13; Length 10; 100.0%; Pred. No. 31; tive 0; Mismatches 0; Indels
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 Mismatches
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                                                                                                                                                                                                                                                                   Cell adhesion inhibitor #1
                                                                                                                                                                                                                                   (first entry)
Conservative
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Local 5; Conserv?
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Gaps
                                                          This peptide deriv. inhibits adhesion of animal cells, partic patelet aggregation. The deriv. can be used in cancer metastasis inhibitors, wound healers, immune inhibitors, platelet aggregation inhibitors or drugs for treating neuropathy.
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llarity 100.0%; Pred. No. 31;
Conservative 0; Mismatches 0; Indels
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Claim 1; Page 1; 9pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide deriv., for cancer metastasis inhibitor - useful as wound healer, immune- and platelet aggregation inhibitor and neuropathy
                                                                                                                                                                                                                                                        platelet aggregation; cell adhesion; cancer metastasis inhibitor; wound healing; immune inhibitor; neuropathy drug.
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             Length 10;
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Pred. No. 31;
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                                     0; Mismatches
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             100.0%;
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            Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1992-401809/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 AA;
                                                                                                                                                                                                                                                                                                                           Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rreating drug
                                                             1 EILDV 5
                                                                                                                                                                                                                                                                                                                                                                            JP04297495-A.
                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAR-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                       21-OCT-1992
                                                                                BILDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 EILDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EILDV
                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                AAR29107;
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                                                                                                                             RESULT 41
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                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                             This peptide deriv. inhibits adhesion of animal cells, partic patelete aggregation. The deriv. can be used in cancer metastasis inhibitors, wound healers, immune inhibitors, platelet aggregation inhibitors or drugs for treating neuropathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This peptide deriv. inhibits adhesion of animal cells, partic patelet aggregation. The deriv. can be used in cancer metastasis inhibitors, wound healers, immune inhibitors, platelet aggregation inhibitors or drugs for treating neuropathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide deriv., for cancer metastasis inhibitor - useful as wound healer, immune- and platelet aggregation inhibitor and neuropathy treating drug
                                                                                                  Peptide deriv., for cancer metastasis inhibitor - useful as wound healer, immune- and platelet aggregation inhibitor and neuropathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     platelet aggregation, cell adhesion, cancer metastasis inhibitor, wound healing, immune inhibitor, neuropathy drug.
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                                                                                                                                                                                                                                                                      100.0%; Score 23; DB 13; Length 10; 100.0%; Pred. No. 31;
                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                     Disclosure; Page 3; 9pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                AAR29106 standard; peptide; 10 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Platelet aggregation inhibitor #3.
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                                                (FUJF ) FUJI PHOTO FILM CO LID
                        91JP-0062148
91JP-0062148
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                                                                                                                                                                                                                                                                                               Conservative
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Best Local Similarity
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                                                                         WPI; 1992-401809/49.
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                                                                                                                                                                                                                                              10 AA
                                                                                                                              treating drug
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26-MAR-1991;
                        26-MAR-1991;
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                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    platelet
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                                                                                                                                                                                                                                                                                                                                                                                        RESULT 40
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The alpha-4 beta-1 (CD49d/CD29, VLA-4) cell adhesion receptor is an active participant in leukocyte trafficking functions. Binding of inflammatory cells to endothelial cells that express the CS-1 portion (AAW01703) of fibronectin on their surfaces can be inhibited by CS-1 peptidomimetic cpds. of minimal length. A minimal essential sequence for
                                                                                                                                                                                                                                                                                                                                                                       This peptide deriv. inhibits adhesion of animal cells, partic pattled aggregation. The deriv. can be used in cancer metastasis inhibitors, wound healers, immune inhibitors, platelet aggregation inhibitors or drugs for treating neuropathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fibronectin; high affinity, CS-1; recognition sequence; VLA-4; plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 plan-4 pl
                                                                                                                                                                                                Peptide deriv., for cancer metastasis inhibitor - useful as wound healer, immune- and platelet aggregation inhibitor and neuropathy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         skin inflammation; central nervous system demyelinating disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 23; DB 13; Length 10; 100.0%; Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Standard peptide for VLA-4 binding assay.
                                                                                                                                                                                                                                                                                                                    Disclosure; Page 3; 9pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW01705 standard; peptide; 10 AA.
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                                                                                   (FUJF ) FUJI PHOTO FILM CO LTD.
                          91JP-0062148.
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93US-0164101
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                                                                                                                                     WPI; 1992-401809/49
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                             26-MAR-1991;
                                                                                                                                                                                                                                                         treating drug
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide deriv., for cancer metastasis inhibitor - useful as wound healer, immune- and platelet aggregation inhibitor and neuropathy
platelet aggregation; cell adhesion; cancer metastasis inhibitor; wound healing; immune inhibitor; neuropathy drug.
                                                                                                                                                                                             /note= "has CH2CH(CH3) (CH2)3CH(CH3) (CH2)3CH(CH3)--(CH2)3CH(CH3)2-CO-
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/note= " has -CH2CH2CH(CH3)(CH2)3CH(CH3)(CH2)3-
-CH(CH3)(CH2)3CH(CH3)2"
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Misc-difference
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specific VLA-4 recognition of CS-1 has been identified as the tripeptide LDV. The generic peptidomimetic inhibits the binding of Jurkat cells (ATCC TIB 152) to a solid phase-bound CS-1 peptide in an in vitro assay in an ag. buffer at a pH value of 7.2-7.4 to an extent that is equal to or upto about 3000-fold greater than the inhibition in the binding exhibited by the present standard peptide sequence. CS-1 mediated inflammation, e.g. asthma, rheumatoid archritis, osteoarthritis, allograft rejection, skin inflammation or central nervous system demyelinating disease, can be treated by the peptidomimetics. See AAW01706-27 for exemplary inhibitor peptides.
                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fibronectin; high affinity; CS-1; recognition sequence; VLA-4; alpha-4 beta-1 cell adhesion receptor; CD49d/CD29; inhibitor; leukocyte trafficking function; peptidomimetic; treatment; asthma; rheumatoid archritis; osteoarchritis; allograft rejection; skin inflammation; central nervous system demyelinating disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inhibitor of fibronectin CS-1 peptide and VLA-4 receptor binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New peptide mimics of fibronectin CS-1 sequence - inhibit interaction of endothelial cells and VLA-4, carrying inflammatory cells, for treating or preventing asthma, arthritis etc.
                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                         100.0%; Score 23; DB,16; Length 10; 100.0%; Pred. No. 31;
                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Page 36; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW01725 standard; peptide; 10 AA.
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93US-0164101,
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                                                                                                                                                                                                                                                                          Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CYTE-) CYTEL CORP.
                                                                                                                                                                                                                     10 AA;
                                                                                                                                                                                                                                                                                                                                    1 BILDV 5
                                                                                                                                                                                                                                                                                                                                                                        3 EILDV 7
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06-DEC-1993;
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                                                                                                                                                                                                                       Sequence
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Vascular cell adhesion molecule-1 (VCAM-1) is protein found on the surface of endothelial cells that line the interior wall of capillaries. VCAM-1 recognises and binds to the integrin alpha-4beta-1 (TAMB1) or VLAM-4 for very late antigen-4), a heterodimeric protein present on the surface of certain white blood cells. Binding of IAAB1 to VCAM-1 allows white blood cells to adhere to the capillary wall in areas where the surface of certain white blood cells in areas where the surface of certain wite capillary has been infected or damaged. Sometimes this white blood cell migration can become uncontrolled, with white blood cells flooding to the scene, causing widespread tissue damage. Cods. capable of blocking this process may be beneficial as therapeutic agents. IAAB1 also recognises the extracellular matrix glycoprotein fibronectin. One site is found in the HeplI region and is a cythin fibronectin. One site is found in the HeplI region and is a leteratively spliced type III connecting segments. CSI has the higher affinity for IAAB1 and contains the tripeptide LDV as its minimal active site. Peptides AAR95704-805 are modeled after a portion of the CSI
                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                           VCAW-1; vascular cell adhesion molecule-1; VLA-4; very late antigen-4; inhibitor; binding; white blood cell; migration; capillary wall; tissue damage; injury; fibronectin; extracellular matrix glycoprotein; CS1; CS5; H1; LDV; active site.
                                                                                                                                     Gapв
inflammation or central nervous system demyelinating disease, can be treated by the peptidomimetics. AAW01706-27 are exemplary inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New peptide(s) based on the LDV domain of fibronectin - used for inhibiting binding of alpha-4, beta-1 integrin to VCAM-1, fibronectin or invasin
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                                                                                                     16; Length 10
                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                              Alpha-4Beta-1 integrin binding inhibitory peptide 101.
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                                                                                                     100.0%; Score 23; DB 100.0%; Pred. No. 31;
                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Column 67-68; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                            AAR95804 standard; peptide; 10 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Thr-NH2"
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                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                   Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1996-221274/22
                                                                     10 AA;
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Modified-site
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                                                                                                                                                                       1 EILDV
                                                                                                                                                                                                3 EILDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                              AAR95804;
                                                                     Sequence
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                                   peptides.
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Matches
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                                    1 EILDV
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                                                                                                                                             AAW71246;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Guences AAW70543 to AAW70545 represent CS-1 peptide fragments used during the course of the invention. The invention provides integrinting the course of the invention. The invention provides integrinting the course of the invention. The invention provides that comprise an integrint alpha or beta claim associated with an immunoglobulin light or heavy chain. These chimeric protein containing an integrint alpha chain and an immunoglobulin chain; the invention of the protein containing an integrinting an integrinting an integrinting an integrinting an integrinting an integrinting an integrinting an integrinting the analyst chain; or one of the two may be a light of the chain is preferably beta 1. Animal cells transformed with vectors containing the DNA coding for the above chimeric proteins can be used in the preparation of the chimeric proteins and their heterodimer complexes. The heterodimer complexes, which are useful for testing potential promoters and inhibitors of the binding of integrins to their configuration as blood platelet substitutes and hemostatics and as
                                                                                    ö
                                                                                                                                                                                                                                                                                       Integrin; alpha-4 chain; immunoglobulin; chimeric; heterodimer complex;
inhibitor; binding; ligand; blood platelet; hemostatic; diagnostic agent;
peptide that include the LDV domain presented in such a way by its novel flanking sequence to produce a potent inhibitor of IA4B1 binding.
                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Integrin-immunoglobulin chimeric protein heterodimer complexes as platelet substitutes - contain the alpha and beta integrin chains associated in stable state and bind to extracellular matrix in the
                                                                                     ö
                                                          100.0%; Score 23; DB 17; Length 10; 100.0%; Pred. No. 31; ove 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                CS-1 peptide fragment 1 (a fibronectin fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 10; Page 30; 87pp; Japanese.
                                                                                                                                                                                          AAW70543 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               presence of plasma components
                                                                                                                                                                                                                                                                                                                                                                                                            98WO-JP00370
                                                                                                                                                                                                                                                                                                                                                                                                                                   97JP-0234544.
                                                                                                                                                                                                                                         (first entry)
                                                (TORA ) TORAY IND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tanaka T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-427881/36.
                                                                                                                                                                                                                                                                                                               CS-1; fibronectin
                                    10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JAN-1997;
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                                                                                                         1 EILDV
                                                                                                                            3 EILDV
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                                    Sequence
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AAW70543
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DB 19; Length 10;

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Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is used in the course of the invention. The specification describes Hepatitis drugs which contain integrin inhibitors include inhibitors as the active ingredient. These integrin inhibitors include antibodies, proteins, polypeptides, peptides, mucleic acids, saccharides, and their derivatives. They also include low molecular weight compounds capable of binding to integrins (e.g. alpha chain type with alpha 1, particularly anti-VLA-4 antibody, VLA-4 inhibiting peptides and low molecular weight VLA-4 inhibiting compounds. The products can be used for treating hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis drug; integrin inhibitor; integrin binding; {\tt VLA-4}; treatment; hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Integrin inhibitors including antibodies, proteins, nucleic acids, saccharide(s), capable of binding to integrin(s) as active ingredient in remedies - for treating hepatitis, by inhibiting cell
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  Indels
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                                                                                                                                                                                                                                                                                                                                                                            Peptide seguence of the invention.
                                                                                                                                                                                                                           AAW71246 standard; Peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW88058 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tanaka T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98WO-JP00802.
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Best Local Similarity 100.00
Crihes 5; Conservative
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  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-480938/41.
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WO200192543-A2
                                              Arrhenius TS,
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                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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Matches
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                                                                                                                                                                                                                                                                                                           The present sequence represents part of a CS-1 peptide. The specification describes a cyclic CS-1 peptidommimetic inhibitor peptide, which is water soluble and inhibits the binding of Jurkat cells to a solid-phase bound peptide (AAW88057). The inhibitor peptides are useful for treating fibronectin CS-1 or sVCAM 1/VLA-4 mediated inflammation, esg. asthmá, arkhritic conditions (e.g. rheumatoid arthritis, osteoarthritis), allograft rejection, skin inflammation and demyelinating diseases of the central nervous system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fibronectin, FN, CS-1, endothelial cell, VLA-4 integrin, alpha-4-beta-1, CD49d/CD29; leukocyte, inflammatory cell, inflammation; cell adhesion, inhibitor; peptidomimetic; autoimmune disease; inflammatory disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                   Cyclic inhibitor peptide - useful for treating fibronectin CS-1 or sVCAM-1/VLA-4 mediated inflammation, e.g. asthma and arthritic
                          Cyclic CS-1 peptidomimmetic inhibitor; Jurkat cell binding; fibronectin CS-1 mediated inflammation; rheumatoid arthritis; SVCAM 1/VLA-4 mediated inflammation, asthma; arthritic condition; rheumatoid arthritis; allograft rejection; CS-1; skin inflammation, demyelinating disease; central nervous system.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pibronectin CS1-derived peptide, SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 23; DB 100.0%; Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                        Example 8; Column 14; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY77412 standard; peptide; 10 AA.
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                                                                                                                                                               95US-0519109.
                                                                                                                                            95US-0519109
                                                                                                                                                                        94US-0296241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                             Arrhenius TS, Elices MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
          CS-1 peptide portion.
                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
ses 5; Conservat
                                                                                                                                                                                                                                  WPI; 1999-152837/13
                                                                                                                                                                                          (CYTE-) CYTEL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                10 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 EILDV 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-DEC-1998;
                                                                                                                                            25-AUG-1995;
                                                                                                                                                               25-AUG-1995;
                                                                                                                                                                        25-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-MAY-2000
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                                                                                                      JS5869448-A
                                                                                                                         09-FEB-1999
                                                                                                                                                                                                                                                                        conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                          BILDV
                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY77412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia.
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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conditions, such as asthma, rheumatoid arthritis, osteoarthritis and allograft rejection. They may also be used to treat psoriasis and other skin inflammations, demyelinating diseases of the central nervous system (e.g., multiple sclerosis), allergies, atherosclerosis, colitis, diabetes, inflammatcory bowel disease, kidney inflammation and restenosis. Prior art inhibition of VLA-4/CS-1 interaction either involves the use of anti-VLA-4 antibodies, which can themselves induce an immune response on repeated administration, or the 25-mer CS-1 peptide, which is large and costly to make and is subject to rapid proteolytic degradation. The peptidomimetics of the invention are smaller in comparison to the CS-1 peptide and therefore less expensive to manufacture, and are resistant to proteolysis. Sequences AAY77411-Y77414 and AAY77434-Y77444 represent fragments of the CS-1 peptide to immobilised CS-1 peptide (AAY77414).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to peptidomimetic compounds (AAY77415-Y77438) capable of inhibiting the binding of the VLA-4 integrin (alpha-4-beta-1, CD494/CD29) to the CS-1 portion (25 amino acids) of a splice variant of the extracellular matrix protein fibronectin (FN). VLA-4 is expressed on the surface of leukocytes; the CS-1 FN/VLA-4 interaction plays an important role in the maturation and trafficking. VLA-4-mediated leukocyte adhesion to the CS-1 FN of endothelial cells is also a critical step in the inflammatory response. The peptidomimetics of the invention may be used to treat both chronic and acute immunoinflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Virucide, human immunodeficiency virus, HIV, cytostatic, ophthalmological, vasotropic, vaccine, gene therapy, transfection, cystic fibrosis, asthma; cancer, leukaemia, glaucoma; gene vaccination, anti-sense therapy, eye disease, corneal organ transplant, integrin,
                                                                                                                                                                                                                                                                       New peptidomimetic compounds used as cell surface fibronectin expressing receptor and VLA-4 inhibitors for treating inflammatory and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gape
                                                                                          Chen PG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
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                                                                                          Huyghe BG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transfection associated, integrin binding peptide #8.
                                                                                          He Y,
                                                                                          Gaeta FCA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; Page 238; 243pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU74984 standard; Peptide; 10 AA.
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                                                                                                                                                                                                                                                                                                                                                                                cardiovascular disorders
                                                                                          Elices
                                                                                                                                                                                     WPI; 2000-182213/16.
(CYTE-) CYTEL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 AA;
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2000GB-0013089 2000GB-0013090,

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30-MAY-2001; 2001WO-GB02394.
                                                                                            01-MAY-2001; 2001US-287410P.
                                                                                                                       (ICHI-) ICH PRODN LTD
                                                                                                                                                                            WPI; 2002-139612/18.
                                                                 30-MAY-2000;
                                                                                 30-MAY-2000;
              06-DEC-2001
                                                                                                                                                 Hart SL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention describes transfecting (I) confluent cells or other slowly dividing or non-dividing cells that are in contact with each other, with a nucleic acid. The method comprises contacting the cells with a receptor-targeted vector comprising the nucleic acid, and an agent that transfecting the cells ding that that transfecting bronchial and lung transfection. (I) is useful for transfecting bronchial and lung cancers and viral infections e.g. human immunodeficiency virus (HIV) infection. Hamaropoietic cell transfection enables gene therapy, gene vaccination and anti-sense therapy of diseases involving haematopoietic cells, including leukaemia and bone marrow stem cell disorders.

Transfection of corneal endothelium is useful for treatment of eye disease affecting the corneal organ transplants, for e.g. in glaucoma. A gene preventing cell proliferation in blood vessel walls is introduced using an integrin targeting transfection vector complex (II) to reduce restenosis. (II) is useful for intracellular transport and delivery of anti-sense oligonuclede, which enables antiviral and cancer therapy and is effective in transporting large DNA molecules. This sequence represents a peptide that lacks the conserved RGD integrin binding amino acid sequence but binds integrins allowing the investice acid to pass into the cell, described in the method of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Integrin binding component; polycationic nucleic acid-binding component;
                                                                                                                                                             Transfecting confluent cells with nucleic acid for gene therapy or gene vaccination, comprises contacting the cells with a receptor-targeted vector having the nucleic acid and an agent that disrupts cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lipid component; prophylaxis; immunisation; antisense therapy; asthma; cystic fibrosis; cancer; viral infection; human immunodeficiency virus; HIV infection; vaccine; neuroblastoma; bone marrow stem cell disorder; leukaemia; adjuvant immunotherapy; eye disease; glaucoma; restenosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            °;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 23; DB 23; Length 10; 100.0%; Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                              Claim 17; Page 17; 111pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE17114 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Integrin-binding peptide #16.
30-MAY-2001; 2001WO-GB02396.
                       30-MAY-2000; 2000GB-0013089.
30-MAY-2000; 2000GB-0013090.
01-MAY-2001; 2001US-287410P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            leukaemia, adjuvant immun
integrin-binding peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                               (ICHI-) ICH PRODN LTD
                                                                                                                                   WPI; 2002-114355/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
tes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 AA;
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                                                                                                                                                                                                    unctions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                         Hart SL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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The invention relates to integrin-targetting vectors having enhanced transfection activity. The vector complex comprises a nucleic acid, an integrin binding component, a polycationic nucleic acid, binding component, a polycationic nucleic acid, binding component and a lipid component. The integrin binding component and a lipid component. The integrin binding component component and a lipid component. The integrin binding element and a spacer element. Complex component asserting in useful for transfecting ocells in vitro or in vivo with a nucleic acid, for transfecting bronchial and lung epithelium and caused in human or a non-human animal by a defect and/or a deficiency in a gene, immunisation and antisense therapy of a human or a non-human animal. It is useful for transfections for cystic fibrosis, asthma and also aracters and viral infections. For example human cancers and viral infections for example human and correct and viral infection. It is also useful as a vaccine or for therapy of neuroblascoma and the effective transfection of primary smooth muscle cells, cardiac myocytes and haematopoietic cells. The mantopoietic cells in and antisense therapy of diseases involving haematopoietic cells. Transfection of a cytokine gene may be used for adjuvant immunotherapy. Transfection of a cytokine gene may be used for adjuvant immunotherapy. Transfection of corneal endothellum is useful for treatment of eye disease affecting the cornea or corneal organ transplants, for example transfection of sessel walls is introduced using complex of the invention to reduce vessel walls is introduced using complex of the invention to reduce the integrin-binding peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                     has
Complex for transfecting cell with nucleic acid for treating, preventing conditions caused by deficiency in a gene in humans, nucleic acid, lipid, integrin binding and polycationic nucleic
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                                                                                                                                                                                                                                  Claim 18; Page 78; 108pp; English.
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Best Local Similarity 100.v.
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                                                                                                                                              acid-binding components
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Gaeta FCA;

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This sequence is a fragment of CS-1 (AAW01703) a high affinity peptide cecognition sequence for VLA-4 within fibronectin. The alpha-4 beta-1 (CD494/CD29, VLA-4) cell adheasion receptor is an active participant in leukocyte trafficking functions. Binding of inflammatory cells to endothelial cells that express the CS-1 portion of FN on their surfaces of minimal length. A minimal essential sequence for specific VLA-4 recognition of CS-1 has been identified as the tripeptide LDV. The generic peptidomimetic inhibite the binding of Jurkat cells (ATCC TIB 152) to a solid phase-bound CS-1 peptide in an in vitro assay in an aq. buffer at a pH value of 7.2-7.4 to an extent that is equal to or upto about 3000-fold greater than the inhibition in the binding exhibited by AAW01705. Deletion mutants of the present sequence were formed and in vitro binding of the peptide CS-1 mediated inflammation, e.g. asthma, rheumatoid archritis, osteoarthritis, allograff rejection, skin inflammation or central nervous system demyelinating disease, can be treated by the peptidomimetics. See AAW01706-27 for exemplary inhibitor peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cyclic CS-1 peptidomimimetic inhibitor; Jurkat cell binding; fibronectin CS-1 mediated inflammation; rheumatoid arthritis; sVCAM 1/VLA-4 mediated inflammation; asthma; arthritic condition; rheumatoid arthritis; osteoarthritis; allograft rejection;
                                                                                                                                                                                                  New peptide mimics of fibronectin CS-1 sequence - inhibit interaction of endothelial cells and VLA-4 carrying inflammatory cells, for treating or preventing asthma, arthritis etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 23; DB 16; Length 12; 100.0%; Pred. No. 38; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           skin inflammation; demyelinating disease; central
                                                                                                                                                                                                                                                                      Disclosure, Page 78; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW88061 standard, peptide; 12 AA
                 94WO-US13943.
                                               94US-0164101.
93US-0164101.
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                                                                                                                                     Elices MJ,
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Les 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B12 peptide sequence.
                                                                                                                                                                      WPI; 1995-224284/29.
                                                                                                  (CYTE-) CYTEL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 AA;
                                                                                                                                     Arrhenius TS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ß
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                                                 02-DEC-1994;
                                                                  06-DEC-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                  AR892534 and AAR92235 represents VLA-4 binding peptides. VLA-4 is also known as alpha4beta1 integrin and CD49d/CD29. VLA-4 binds to the con-matrix molecule VCAM-1, which is expressed by endothelial and other cells. This sequence (and peptides designed from it) minic a short cells. This sequence in the heavy chain complementarity determining region (CDR) as of monoclonal antibodies against alpha4beta1 integrin. This sequence inhibits the adhesion of loucocytes mediated by VLA-4. It is useful for treating inflammatory brain disprders (especially multiple clerosclerosis, meningitis, encephalitis, asthma, Alzhaimer's disease, atherosclerosis, AIDS dementia, diabetes, inflammatory bowel disease, theumatoid arthritis, transplant rejection, tumour metastases and creating in sequence can also be labelled, and can then be used for in vivo or in vitro diagnosis, such as monitoring inflammatory responses, isolating leucocytes, in assays for inhibitors of VLA-4/VCAM-1 interactions and imaging sites of inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                 rheumatoid arthritis; transplant rejection; myocardial ischaemia; asthma
diabetes; inflammatory bowel disease; tumour metastases;
                                                                                                                                                                                                                                                                                                                                       - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                   esp. for treatment of inflammatory disease, e.g. multiple sclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fibronectin, high affinity, CS-1, recognition sequence, VLA-4, alpha-4 beta-1 cell adhesion receptor; CD49d/CD29; inhibitor; leukocyte trafficking function; peptidomimetic; treatment; asthma; rheumatoid archritis; osteoarchritis; allograft rejection; skin inflammation; central nervous system demyelinating disease.
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                                                                                                                                                                                                                                                                                                                                       New peptide(s) that bind VLA-4, inhibit leucocyte adhesion
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                                                                                                                                                                                                                                                                      Yednock TA;
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94US-0273055.
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les 5; Conservat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 AA;
AIDS dementia;
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                                                                                WO9601644-A1
                                                                                                                                                   10-JUL-1995;
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11-JUL-1994;
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                                                                                                                 25-JAN-1996
                                                                                                                                                                                                                                                                      Pleiss MA,
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                                                 Synthetic.
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                                                                                                                                                                   The specification describes a cyclic CS-1 peptidomimimetic inhibitor which is water soluble and inhibits the binding of Jurkat cells to a solid-phase bound peptide (AAM88057). The inhibitor peptides are useful for treating fibronectin CS-1 or sVCAM I/VIA-4 mediated inflammation, e.g. asthma, arthritic conditions (e.g. rheumatoid arthritis, oslograft rejection, skin inflammation and demyelinating diseases of the central nervous system. The present sequence appears in the specification.
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                               Cyclic inhibitor peptide - useful for treating fibronectin CS-1 or sVCAM-1/VLA-4 mediated inflammation, e.g. asthma and arthritic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New integrin-targeting transfection complex including lipid - used to improve transfection efficiency for a very wide range of cells, useful in, e.g. antisense therapy and genetic immunisation
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                                                                                                                                                                                                                                                                                                        100.0%; Score 23; DB 20; Length 12; 100.0%; Pred. No. 38; 0; Indels iive 0; Mismatches 0; Indels
                                                Tempczyk A, Zheng Z;
                                                                                                                                             Disclosure; Columns 77-78; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 restenosis; leukaemia; asthma; glaucoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW95414 standard; peptide; 12 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 12; Page 50; 70pp; English.
94US-0296241
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                                              Arrhenius TS, Elices MJ,
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                                                                                                                                                                                                                                                                                                                      Local Similarity 100.
ses 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Integrin-binding peptide
                                                                       WPI; 1999-152837/13.
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                        (CYTE-) CYTEL CORP.
                                                                                                                                                                                                                                                                                  12 AA;
                                                                                              Cyclic inhibitor
25-AUG-1994;
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                                                                                                                                                                                                                                                                                    Sequence
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The invention relates to an integrin-targeting transfection complex. The complex comprises a nucleic acid, an integrin-binding component, a

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polycationic nucleic acid-binding component and a lipid. The complexes are used for in vivo or in vitro transfection of cells, specifically:

(1) for treatment or prevention of disease (in humans or other animals) caused by defective or deficient genes; (ii) for immunisation; (iii) for antisense therapy, and (iv) for protein production in host cells, e.g. or enzymes, therapeutic agents, vacainating immunogens and diagnostic antisens. Typical of the diseases that can be treated or prevented are cystic fibrosis, cancer, viral infection (e.g. human immunodeficiency irus), cardiovascular disease (e.g. restenosis), leuksemia, asthma and glaucoma. Incorporation of the lipid into the complex increases transfection levels from 1-10 percent to over 50 percent. This effect is observed with all cell types tested including those that are resistant to transfection by most plasmid vectors. The complexes can carry large genes, up to 125 kb, e.g. an artificial chromosome. The present sequence represents a claimed example of an integrin-binding peptide used in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fibronectin, FN; CS-1; endothelial cell; VLA-4 integrin; alpha-4-beta-1; CD49d/CD29; leukocyte; inflammatory cell; inflammation; cell adhesion; inhibitor; peptidomimetic; autoimmune disease; inflammatory disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to peptidomimetic compounds (AAY77415-Y77438) capable of inhibiting the binding of the VLA-4 integrin (alpha-4-beta-1, 4.2 by 494/CD29) to the CS-1 portion (52 amino acids) of a splice variant of the extracellular matrix protein fibronectin (FN). VLA-4 is expressed on the surface of leukocytes; the CS-1 FN/VLA-4 interaction plays an important role in the maturation and trafficking. VLA-4-mediated leukocyte adhesion to the CS-1 FN of endothelial cells is also critical step in the inflammatory response. The peptidomimetics of the invention may be used to treat both chronic and acute immunoinflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New peptidomimetic compounds used as cell surface fibronectin expressing receptor and VLA-4 inhibitors for treating inflammatory and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fibronectin CS1-derived peptide, SEQ ID NO:2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 238; 243pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expressing receptor and V
cardiovascular disorders
                                                                                                                                                                                                                                                                                                                                                                           transfection complexes.
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                                                                                                                                                                                                                                                                                                                                                                                                                        12 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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              allograft rejection. They may also be used to treat psoriasis and other skin inflammations, demyelinating diseases of the central nervous system (e.g., multiple sclerosis, allorgies, atherosclerosis, colitis, diabetes, inflammatory bowel disease, kidney inflammation mether restenosis. Prior art inhibition of VLA-4/CS-1 interaction either immoves the use of anti-VLA-4 antibodies, which can themselves induce an immone response on repeated administration, or the 25-mer CS-1 peptide, which is large and costly to make and is subject to rapid proteolytic comparison to the CS-1 peptide and therefore less expensive to manufacture, and are resistant to proteolysis. Sequences AAY77411-Y77414 and AAY7743-Y77444 represent fragments of the CS-1 peptide for their ability to inhibit VLA-4 Jurkat cells to immobilised CS-1 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention describes transfecting (I) confluent cells or other slowly dividing or non-dividing cells that are in contact with each other, with a nucleic acid. The method comprises contacting the cells with a receptor-targeted vector comprising the nucleic acid, and an agent that disrupts cell-cell junctions under conditions suitable to effect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Virucide, human immunodeficiency virus, HIV, cytostatic, ophthalmological, vasotropic, vaccine; gene therapy, transfection; cystic fibrosis; asthma; cancer; leukaemia; glaucoma; gene vaccination, anti-sense therapy; eye disease; corneal organ transplant; integrin; transfection; restenosis; alpha 4 beta 1 integrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transfecting confluent cells with nucleic acid for gene therapy or gene vaccination, comprises contacting the cells with a receptor-targeted vector having the nucleic acid and an agent that disrupts cell-cell
such as asthma, rheumatoid arthritis, osteoarthritis and
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                                                                                                                                                                                                                                                                                           21; Length 12;
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                                                                                                                                                                                                                                                                                                                         0; Indels
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30-MAY-2000; 2000GB-0013090.
01-MAY-2001; 2001US-287410P.
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                                                                                                                                                                                                                                                                                                                         Conservative
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Best Local Similarity
5; Conserve
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                                                                                                                                                                                                                                                            12 AA;
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transfection. (I) is useful for transfecting bronchial and lung epithelium for gene therapy for cystic fibrosis, asthma and also various cancers and viral infections e.g. human immundeficacy virus (HIV) infections e.g. human immundeficacy virus (HIV) infection. Haematopoietic cell transfection enables gene therapy, gene vaccination and anti-sense therapy of disease involving haematopoietic cells, including leukaemia and bone marrow atem cell disorders.

Transfection of corneal endothelium is useful for treatment of eye disease affecting the cornea or corneal organ transplants, for e.g. in glacomea. Agene preventing cell proliferation in blood vessel walls is introduced using an integrin transfection in blood vessel walls is introduced using an integrin transporting transfection vector complex (II) to reduce restenosis. (II) is useful for intracellular transport and cancer therapy and is effective in transporting large DNA molecules. This sequence represents a peptide that lacks the conserved RGD annot call sequence and cysteine residues for cyclisation, but can bind to integrins to allow the nucleic acid to pass into the cell, described in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Integrin binding component; polycationic nucleic acid-binding component; lipid component; prophylaxis; immunisation; antisense therapy; asthma; cystic fibrosis; cancer; viral infection; human immunodeficiency virus; HIV infection; vaccine; neuroblastoma; bone marrow stem cell disorder; leukaemia; adjuvant immunotherapy; eye disease; glaucoma; restenosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gapa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complex for transfecting cell with nucleic acid for treating, preventing conditions caused by deficiency in a gene in humans, has nucleic acid, lipid, integrin binding and polycationic nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 23; DB 23; Length 12; 100.0%; Pred. No. 38;
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30-MAY-2000; 2000GB-0013090.
01-MAY-2001; 2001US-287410P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Integrin-binding peptide 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                              12 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EILDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE17104;
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hart SL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ß
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE17104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
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This represents a CS-1 peptide sequence. The invention provides connegrin-immunoglobulin chimeric protein heterodimer complexes that comprise an integrin alpha or beta chain associated with an immunoglobulin light or heavy chain. These chimeric proteins form containing an integrin batticular with a chimeric protein containing an integrin beta chain and an immunoglobulin chain in each case may be a heavy chain, or one of the two may be a light chain. The integrin alpha chain is preferably alpha 4 cor alpha 2 and the integrin alpha chain is preferably beta 1. Animal cells two may be a light chain. The integrin alpha chain is preferably alpha 4 cor alpha 2 and the integrin beta chain is preferably beta 1. Animal cells transformed with vectors containing the DNA coding for the above chimeric proteins can be used in the preparation of the chimeric proteins and their theterodimer complexes. The heterodimer complexes, which are useful for testing potential promoters and inhibitors of the binding of integrins to their ligands, function as blood platelet substitutes and hemostatics and as diagnostic agents.

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an integrin binding component, a polycationic nucleic acid-binding component and a lipid component. The integrin binding component comprises an integrin-binding element and a spacer element. Complex of the invention is useful for transfecting cells in vitro or in vivo with a nucleic acid, for treatment or prophylaxis of a condition caused in human or a non-human animal by a defect and/or a deficiency in a gene, immunisation and antisense therapy of a human or a non-human animal. It is useful for transfecting bronchial and lung epithelium and corneal endothelium for gene therapy for cystic fibrosis, asthma and also various cancers and viral infections. The also useful as a vaccine corneal endothelium for gene therapy for cystic fibrosis, asthma and immunodeficiency virus (HIV) infection. It is also useful as a vaccine or for therapy of neuroblastoma and the effective transfection of primary smooth muscle cells, cardiac myocytes and haematopoietic cells. Heematopoietic cell transfection enables gene therapy, gene vaccination and antisense therapy of diseases involving haematopoietic cells. Including leukaemia and bone marrow stem cell disorders, for example transfection of corneal endothelium is useful for treatment of eye disease affecting the cornea or corneal organ transplants, for example in glaucoma. A gene that prevents proliferation of cells in blood vessel walls is introduced using complex of the invention to reduce restenosis. The present sequence is integrin-binding peptide

cetterosis. The present sequence is integrin-binding peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Integrin; alpha-4 chain; immunoglobulin; chimeric; heterodimer complex;
inhibitor; binding; ligand; blood platelet; hemostatic; diagnostic agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 23; DB 23; Length 12; 100.0%; Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CS-1 peptide sequence (a fibronectin fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW70541 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CS-1; fibronectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EILDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EILDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW70541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 60
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Gaps

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Indels

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0, Mismatches

5; Conservative

Matches

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1 EILDV

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Best Local Similarity

13 AA;

Sequence Query Match AAW71245 standard; Peptide; 13 AA.

RESULT 61

AAW71245;

100.0%; Score 23; DB 19; Length 13; 100.0%; Pred. No. 42;

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The present sequence is used in the course of the invention. The specification describes Hepatitis drugs which contain integrin inhibitors as the active ingredient. These integrin inhibitors include antibodies, proteins, polypeptides, peptides, nucleic acids, saccharides, and their derivatives. They also include low molecular weight compounds alpha 2, etc., or beta chain type with beta 1, particularly anti-VLA-4 antibody, VLA-4 inhibiting peptides and low molecular weight VLA-4 inhibiting compounds. The products can be used
                                                                                    Hepatitis drug; integrin inhibitor; integrin binding; VLA-4; treatment;
                                                                                                                                                                                                                                                                                                                                                                                    active
inhibiting cell
                                                                                                                                                                                                                                                                                                                                                                    nucleic acids,
                                                                                                                                                                                                                                                                                                                                                                  Integrin inhibitors including antibodies, proteins, saccharide(s), capable of binding to integrin(s) as ingredient in remedies - for treating hepatitis, by
                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Page 16; 35pp; Japanese.
                                                        Peptide sequence of the invention.
                                                                                                                                                                                                                                                                                                           Tanaka T;
                                                                                                                                                                                                                     98WO-JP00802.
                                                                                                                                                                                                                                                   97JP-0042493.
                             18-NOV-1998 (first entry)
                                                                                                                                                                                                                                                                                (TORA ) TORAY IND INC
                                                                                                                                                                                                                                                                                                             Moriya K,
                                                                                                                                                                                                                                                                                                                                       WPI; 1998-480938/41.
                                                                                                                                                           W09837914-A1
                                                                                                                                                                                                                     26-FEB-1998;
                                                                                                                                                                                                                                                   26-FEB-1997;
                                                                                                                                                                                        03-SEP-1998
                                                                                                   hepatitis.
                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                             Kainoh M,
                                                                                                                                                                                                                                                                                                                                                                                                                 adhesion
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Integrin-immunoglobulin chimeric protein heterodimer complexes as platelet substitutes - contain the alpha and beta integrin chains associated in stable state and bind to extracellular matrix in the

98WO-JP00370 97JP-0234544 97JP-0015118

29-JAN-1998;

29-AUG-1997; 29-JAN-1997;

WO9832771-A1

30-JUL-1998.

(TORA) TORAY IND INC.

Tanaka T;

Kainoh M,

NPI; 1998-427881/36.

Claim 41; Page 25; 87pp; Japanese.

presence of plasma components

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as very late antigen-4 (VLA-4) antagonists to treat diseases mediated by cell adhesion. (I) has antiasthmatic, antiallergic, antifilammatory, neuroprotective and antiarteriosclerotic activities. (I) are used to prevent the action of VLA-4 in prevention and treatment of diseases mediated by cell adhesion selected from asthma, allergic rhinitis, multiple sclerosis, atherosclerosis and inflammatory bowel disease. The present sequence represents a synthetic CS-1 peptide which is used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Very late antigen-4; VLA-4; cell adhesion inhibitor; CD49d/CD29; alpha4/beta7 integrin; cyclic amidine derivative, rhinitis; asthma; multiple sclerosis; atherosclerosis; bowel disease; inflammation; nephritis; AIDS-related dementia; acquired immunodeficiency syndrome; diabetes; conjunctivitis; Alzheimer & disease; acrtic stenosis; myeloma; contact dermal hypersensitivit; ulcerative colitis; Crohn's disease; lung disease; cancer; viral infection; meningitis; pulmonary fibrosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes heterocyclic amides (I) which are used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Use of new and known heterocyclic amides as VLA-4 antagonists to treat and prevent disorders mediated by cell adhesion e.g. asthma, allergic rhinitis, multiple sclerosis, atherosclerosis and inflammatory bowel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  myocarditis; organ transplantation; psoriasis; restenosis; retinitis;
arthritis; stroke; tumour metastasis; uveititis; vascular occlusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Very late antigen-4 (VLA-4) dependent adhesion related peptide, CS-1.
                                                                                          Heterocyclic amide; cell adhesion inhibitor; very late antigen-4; VLA-4 antesponier; antiasthmatic; antialriammatory; vola-quesponier; antiarteriosclerotic; asthma; allemustory neuroprotective; antiarteriosclerotic; asthma; allergic rhinitis; multiple sclerosis; atherosclerosis; inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 23; DB 22; Length 13; 100.0%; Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                      Chang LL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 198; Page 148; 169pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                      Doherty G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU77526 standard; Peptide; 13 AA.
                                                                                                                                                                                                                                                                                                        14-AUG-2000; 2000WO-US22115.
                                                                                                                                                                                                                                                                                                                                           99US-0149042.
                                                                                                                                                                                                                                                                                                                                                                                                                      Delaszlo SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                               (MERI ) MERCK & CO INC.
                                                       Synthetic CS-1 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-168836/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                             WO200112183-A1.
                                                                                                                                                                                                                                                                                                                                           16-AUG-1999;
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                   16-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                    Hagmann WK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EILDV
                                                                                                                                                                                         Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        are cyclised via disulphide or amide bonds. The peptides are very late antigen-4 (VLA-4) adhesion inhibitors. They are useful for treating inflammation, especially allergic inflammation and hepatitis, autoimmune disease, rejection reactions following organ transplants, type I diabetes, Crohn's disease, post-surgical restenosis and arteriosclerosis. The present sequence is used in the course of
                                                                                                                                                                                                                                                                                                                                                                                                                                    Cyclic hexapeptide; very late antigen-4; VLA-4; adhesion inhibitor; inflammation; allergic inflammation; hepatitis; autoimmune disease; rejection reaction; organ transplant; type I diabetes; Crohn's disease; post-surgical restenosis; arteriosclerosis.
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                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New cyclic hexapeptides for treating inflammation and hepatitis
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                                                                           19; Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The specification describes cyclic hexapeptides which are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Takeshige H,
                                                                         DB 42;
                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                           100.0%; Score 23; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 4; Page 20; 45pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Takahashi T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB70683 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                    AAY22632 standard, peptide, 13 AA
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                                                                                                                                                                                                                                                                                                                                                             (first entry)
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1es 5; Conservative
                                                                                                                Conservative
for treating hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID 57 of WO9925731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TORA ) TORAY IND INC.
                                                       Query Match
Best Local Similarity
5; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saito N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-370745/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 AA;
                                       13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the invention.
                                                                                                                                                                                     Eilby 10
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                                                                                                                                                                                                                                                                                                                                                             12-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-MAY-1999
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                                                                                                                                                  1 BILDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kainoh M,
                                                                                                                                                                                                                                                                                                                         AAY22632;
                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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RESULT 63 AAB70683 ID AAB7 XX AC AAB7

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This invention relates to the use of a peptide, which is an immunogenic portion derived from a dnaJ heat shock protein (hsp) in modulating an immunome response in a subject. The peptides of the invention may have immunomedulatory, cytostatic, antiinflammatory, antibacterial or antiarthritic properties and can stimulate expression of interleukins, tumour necrosis factor and transforming growth factor beta. The immunogenic peptide is useful for modulating (i.e. augmenting/inducing or reducing/inhibiting) an immune response in a subject having an immunological disorder (e.g. autoimmune disease such as arthritis or articular juvenile idiopathic arthritis), an infectious disease, an inflammatory bowel disease or cancer. The immunogenic peptide of the invention is also useful for modulating immunogenic peptide of the invention is abbject. The immunogenic peptide of the invention a subject. The immunogenic peptide of the above-mentioned diseases in mammals, e.g. cat, dog, horse, farm animal (e.g. ovine, bovine or porcine) or human. In general, the peptide is useful in methods involving mucosal colerisation, DNA vaccination, anergy induction or active immunogenic peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                          treating immunological disorder in subjects such as humans, e.g.
autoimmune disease (e.g. arthritis), infectious disease, inflammatory
                                                                                                                                                                                                                                                                                                                                                                  New immunomodulatory peptides from heat shock proteins, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 23; DB 23; Length 15; 100.0%; Pred. No. 49;
                                                                                                                                                                                                                                                                           Prakken BJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Triazine; polyethylene glycol; agglutination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                           Carson DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR29632 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 10; Page 56; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adhesion inhibitor peptide #2.
                                                                                                                31-OCT-2001; 2001WO-US45344..
                                                                                                                                                             01-NOV-2000; 2000US-245181P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90JP-0316441.
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nes 5; Conservative
                                                                                                                                                                                                       (REGC ) UNIV CALIFORNIA (MART/) MARTINI A.
                                                                                                                                                                                                                                                                                                                                                                                                                                      bowel disease or cancer
                                                                                                                                                                                                                                                                         Albani S,
                                                                                                                                                                                                                                                                                                                   WPI; 2002-489999/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 AA;
                       WO200236611-A2.
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                                                                    10-MAY-2002
                                                                                                                                                                                                                                                                           Martini A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EILDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S EILDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention describes novel substituted cyclic amidine derivatives (I).

(I) are useful for the prevention or treatment of disease or disorders mediated by cell adhesion in a mammal e.g. asthma, allergic rhinitis, multiple sclerosis, atherosclerosis, inflammatory bowel disease or inflammation e.g. acute respiratory distress syndrome (ARDS).

AIDS-related dementia, allergic conjunctivitis, Alzheimer's disease, actic stenosis, autologous bone marrow transplantation, certain types of toxic and immune based nephritis, contact dermal hypersensitivity, ulcerative collitis, Crohn's disease, inflammatory lung disease, inflammatory sequelae of viral infections, meningitis, multiple myeloma, myocarditis, organ transplantation, psoriaais, pulmonary fibrosis, restenosis, retinitis, rheumatoid arthritis, septic arthritis, stroke, concert, tumour metastasis, uveititis, type I diabetes and vascular occlusion following angioplasty. The compound inhibits cell adhesion processes including cell activation, migration, proliferation and the inhibition of very late antigen-4 (VLA-4, CD49d/CD29 or alpha4/beta7 integrin) dependent adhesion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunogenic peptide; heat shock protein; HSP; DNAJ; immunomodulatory; cytoëratic; antiinflammatory; antibacterial; antiarthritic; human; autoimmune disease; arthritis; articular juvenile idiopathic arthritis; inflammatory bowel disease; cancer; HSJI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       New substituted cyclic amidine derivatives for the prevention or treatment of disease mediated by cell adhesion in a mammal e.g. asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 23; DB 23; Length 13; 100.0%; Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mucosal tolerisation; DNA vaccination; anergy induction
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; Page 16; 22pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU98858 standard; Peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                  Shah S;
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                                                                                                                                                                             21-MAY-2001; 2001US-0862194.
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                  Hagmann WK, Doherty GA,
                                                                                                                                                                                                                                                                       (HAGM/) HAGMANN W K.
(DOHE/) DOHERTY G A.
                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-215831/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 AA;
                                                                                         US2002010199-A1.
                                                                                                                                                                                                                                                                                                                   (SHAH/) SHAH S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 EILDV 10
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                                                                                                                                     24-JAN-2002.
angioplasty
                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence
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Gaps

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Indels

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Gaps

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C Y 1 = YC domain;

(L'1) - c-P'1-(L'2) d-PP^2-(L'3) e-P^3 or

(L'1) - c-P'1-(L'2) d-PP^2-(L'3) e-P^3 or

(L'1) - c-P'1-(L'2) d-PP-2-(L'3) e-P^3 or

(L'1) - c-P'1-(L'2) d-PP-2-(L'3) e-P^3 or

(L'1) - c-P'1-(L'2) d-PP-2-(L'3) e-P^3 or

(L'1) - d = same or different [1],

(L'1-L'4 = same or different linkers,

a f = 0 or 1, provided at least one of a and b = 1,

L'1-L'4 = same or different linkers,

a recleic acid that encodes (Ia), an expression vector containing the

nucleic acid that encodes (Ia), an expression or ector containing the

nucleic acid, host cells containing the vector, producing at least one

pharmaceutically active compound (B) by covalently linking at least one

pharmaceutically active compound (B) by covalently linking at least one

C domain to at least one amino acid sequence of a selected randomized

(I) and any of six laminin-related peptides (Ib). The compositions are

used prophylactically and therapeutically in the same way as (I), e.g. to

inhibit platelet aggregation or angiogenesis (tumours), or to treat

inflammation and autoimmune diseases (e.g. rheumatcid arthritis) and many

different forms of osteoporosis, also for diagnosis. Attaching the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a composition comprising an integrin/adhesion antagonistic peptide (I) and a vehicle e.g. IgG Fc. The peptides are based on laminin or saw-scaled viper echistatin and target integrin, selectin or vinculin. Also included are compounds of formula (Ia) and their multimers (\chi^2)_{-} a +F^1-(\chi^2)_{-} b where,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Composition comprising integrin or adhesion antagonistic peptide and vehicle, useful for treating or preventing platelet aggregation, has a longer half-life than free peptide
                                                                                                                                                                                                                                                                                                                                                                                                    antiinflammatory; immunosuppressive; osteopathic; antagonist; laminin; saw-scaled viper; echistatin; integrin; selectin; vinculin; platelet aggregation; anglogenesis; tumour; inflammation; autoimmune disease; rheumatoid arthritis; osteoporosis.
                                                                  13; Length 16,
                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                      IgG Fc; anticoagulant; thrombolytic; cytostatic;
                                                                DB
53;
inhibitors or drugs for treating neuropathy
                                                                                               Mismatches
                                                              Score 23;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boone TC;
                                                                                                                                                                                                                                                  AAU81181 standard; Peptide; 19 AA.
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                                                                100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                     Laminin-related peptide #12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-APR-2000; 2000US-198919P. 03-MAY-2000; 2000US-201394P.
                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-062025/08
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                                                                Query Match
Best Local Similarity
Matches 5; Conserv
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                                 16 AA;
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                                                                                                                                EILDV
                                                                                                                                                              EILDV
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                                 Sequence
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                                                                                                                                                                                                           One of 1 or 2 of these chains are attached via the N- or C-terminal to a 2,46-trisubstituted s-triazine ring, where one substitution is a polyethylene glycol chain [CH3(OCH2CH2)n-O- (in=1-150)] and the other is either another, same, polyechylene glycol chain, or another, same, peptide chain. These PEG derivates or their salts are useful as animal cell adhesion inhibitors, or as platelet agglutination or adhesion inhibitors. They may also be used as carcinoma metastasis inhibitors, wound healing drugs and immunoregulators.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This peptide deriv. inhibits adhesion of animal cells, partic platelet aggregation. The deriv. can be used in cancer metastasis inhibitors, wound healers, immune inhibitors, platelet aggregation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide deriv., for cancer metastasis inhibitor - useful as wound healer, immune- and platelet aggregation inhibitor and neuropathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          platelet aggregation; cell adhesion; cancer metastasis inhibitor; wound healing; immune inhibitor; neuropathy drug.
                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                             New peptide(s) contg. PEG derivs. - are cell adhesion and platelet adhesion inhibitors, useful as carcinoma metastasis inhibitors, immuno-regulators and for wound healing
                                                                                                                                                                                                                                                                                                                                                                                                       DB 13; Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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0; Mismatches
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                                                                                                                                                                              Disclosure, Page 3; 11pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Platelet aggregation inhibitor #7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 3; 9pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR29104 standard; peptide; 16 AA.
                                               (FUJF ) FUJI PHOTO FILM CO LID
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               90JP-0316441.
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                      16 AA;
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               21-NOV-1990;
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WO200181377-A2.
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                                                                                                                            1 EILDV
                                                                                                                                                                                                                                                                                                                                                   Synthetic.
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                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a-f = 0 or 1, provided at least one of a and b = 1, a nucleic acid that encodes [1a], an expression vector containing the nucleic acid, host cells containing the vector, producing a pharmaceutically active compound (B) by covalently linking at least one Fc domain to at least one amino acid sequence of a selected randomized [1] and any of shy lamin-related peptides [1b]. The compositions are insed prophylactically and therapeutically in the same way as [1], e.g. to inhibit platelet aggregation or angiogenesis (tumours), or to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             integrin,
  the half-life (free (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a composition comprising an integrin/adhesion antagonistic peptide (I) and a vehicle e.g. IgG Fc. The peptides are based on laminin or saw-scaled viper echistatin and target integrin selectin or vinculin. Also included are compounds of formula (Ia) and their multimers (X^2)_a - F^2 - (X^2)_b where;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Composition comprising integrin or adhesion antagonistic peptide and vehicle, useful for treating or preventing platelet aggregation, has a longer half-life than free peptide
                                                                                    Gaps
                                                                                                                                                                                                                                                             IgG Fc, anticoagulant, thrombolytic, cytostatic, antagonist, antiinflammatory; immunosuppressive; osteopathic; antagonist, laminin; saw-scaled viper; echistatin; integrin; selectin; vinculin; platelet aggregation; anglogenesis; tumour; inflammation; autoimmune disease; rheumatoid arthritis; osteoporosis.
vehicle (especially Fc domain) to (I) increases the half-life (frare normally degraded very quickly in vivo). The present sequence is an antagonist peptide of the invention.
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                                                               DB 23; Length 19;
                                                                                   0; Indels
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                                                                                   0; Mismatches
                                                              100.0%; Score 23;
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                                                                                                                                                                             AAU81184 standard; Peptide; 19 AA
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                                                                                                                                                                                                                                                                                                                                                                                                              21-APR-2000; 2000US-198919P.
03-MAY-2000; 2000US-201394P.
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                                                                                                                                                                                                                                            Laminin-related peptide #15
                                                                                                                                                                                                                       (first entry)
                                                    Query Match
Best Local Similarity 100.0
These 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                             (AMGE-) AMGEN INC
                                          19 AA;
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AAU81184
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inflammation and autoimmune diseases (e.g. rheumatoid arthritis) and many different forms of osteoporosis, also for diagnosis. Attaching the vehicle (especially Fc domain) to (I) increases the half-life (free (I) are normally degraded very quickly in vivo). The present sequence is an antagonist peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a composition comprising an integrin/adhesion antagonistic peptide (I) and a vehicle e.g. IgG Fc. The peptides are based on laminin or saw-scaled viper echistatin and target integrin, selectin or vinculin.Also incoluded are compounds of formula (Ia) and their miltimers (X'1)_a-F'1-(X^2)_b where,
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                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                          23; Length 19;
                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     r.1 and r.2 and r.2 d.p. r. (L.1) c-p^1, (L.1) c-p^1-(L.2) d-p^2, (L.1) c-p^1-(L.2) d-p^2, (L.1) c-p^1-(L.2) d-p^2-(L.3) e-p^3 or (L.1) c-p^1-(L.2) d-p^2-(L.3) e-p^3-(L.4) E-p^4; p^2-p^4 = same or different (1); L.4 = same or different linkers;
                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IgG Fc; anticoagulant; thrombolytic; cytostatic;
                                                                                                                                                                                                                                                                      DB
64;
                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                          Score 23;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ĮĊ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU81185 standard; Peptide; 19 AA
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                                                                                                                                                                                                                                                                      100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Laminin-related peptide #16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-APR-2001; 2001WO-US13069.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-APR-2000; 2000US-198919P. 03-MAY-2000; 2000US-201394P.
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                                                                                                                                                                                                                                    Query Match
Best Local Similarity 10v...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    = Fc domain;
                                                                                                                                                                                                         19 AA;
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used prophylactically and therapeutically in the same way as (I), e.g. to inhibit platelet aggregation or angiogenesis (tumours), or to treat inflammation and autoimmune diseases (e.g. rheumatoid arthritis) and different forms of osteoporosis, also for diagnosis. Attaching the vehicle (sepecially FC domain) to (I) increases the half-life (free (I) are normally degraded very quickly in vivo). The present sequence is an antagonist peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The peptide is an example of a cell adhesion polypeptide contg. the amino sequence X-Asp-Y-(A)n-Phe, where X and Y = Ala, Leu, Ile or Val. A= any amino acid and n= 3-10. At least a subsequence of the polypeptide is adherent for MoLT-4 human lymphoblastic leukaemia, A375-SM human metastatic melanoma or H1080 human fibrosarcoma cells. The call adhesion peptides are used to modify or control the adhesive properties of cells, e.g. in treatment of inflammatory conditions such as rheumatoid arthritis, asthma, sepsis, graft rejection, inflammatory bowel disease, reperfusion of cardiac tissue after myocardial infarction, and coagulatory disorders. They are selective antagonists of cell adhesion, e.g. they promote adhesion of the speccified cells but inhibit adhesion to the natural adhesion
                                                                                                                                                           Gaps
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/note= "LDV region followed by Phe at position 17."
                                                                                                                                                                                                                                                                                                                                                                          MOLT-4; human; lymphoblastic leukaemia; A375-SM; metastatíc; melanoma; H1080; fibrosarcoma; LDV; LDL; IDA; inflammatory disease; rheumatoid arthritis; asthma; sepsis; graft rejection; reperfusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New cell adhesion (poly)peptide(s) modifying cell adhesive
properties - useful in treating inflammatory conditions e.g.
rheumatoid arthritis, asthma, inflammatory bowel disease, sepsis,
                                                                                                                                                           ö
                                                                                                                               Query Match

100.0%; Score 23; DB 23; Length 19;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Page 4; 23pp; English.
                                                                                                                                                                                                                                                                        AAR26821 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYMA-) UNIV VICTORIA MANCHESTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92WO-GB00226.
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91GB-0002818.
                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                   Cell adhesion polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1992-299988/36.
                                                                                                         19 AA;
                                                                                                                                                                                                         10 EILDV 14
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                                                                                                                                                                                  1 BILDV 5
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                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                  AAR26821;
                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                RESULT 71
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                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The peptide is an example of a cell adhesion polypeptide contg. the amino sequence X-Asp-Y-(A)n-Phe, where X and Y = Ala, Leu, Ile or Val, As any amino acid and n= 3-10. At least a subsequence of the polypeptide is adherent for MOLT-4 human lymphoblastic leukaemia, A375-SM human metastatic melanoma or H1080 human fibrosarcoma cells. The cell adhesion peptides are used to modify or control the adhesive properties of cells, e.g. in treatment of inflammatory conditions such as rheumatoid arthritis, asthma, sepsis, graft rejection, inflammatory bowel disease, reperfusion of cardiac tissue after myocardial infarction, and coagulatory disorders. They are selective antagonists of cell adhesion, e.g. they promote adhesion of the speccified cells but inhibit adhesion to the natural adhesion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLT-4; human; lymphoblastic leukaemia; A375-SM; metastatic; melanoma; H1080; fibrosarcoma; LDV; LDL; IDA; inflammatory disease; rheumatoid arthritis; asthma; sepsis; graft rejection; reperfusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New cell adhesion (poly)peptide(s) modifying cell adhesive
properties - useful in treating inflammatory conditions e.g.
rheumatoid arthritis, asthma, inflammatory bowel disease, sepsis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
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                                                                                                                                Score 23; DB 13; Length 20;
Pred. No. 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IndelB
                                                                                                                                                                                     Indels
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                                                                                                                                                                                     0; Mismatches
protein contg. the adhesive sequence. See also AAR26822-30 and AAR30887-903.
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See also AAR26821-30 and AAR30887-903.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 11; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR30901 standard; peptide; 20 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell adhesion polypeptide CS12.
                                                                                                                                100.0%;
100.0%;
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91GB-0002818.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-FEB-1993 (first entry)
                                                                                                                                                                                     5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1992-299988/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                            Best_Local Similarity
Matches 5; Conser
                                                                              20 AA;
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                                                                                                                                                                                                                                          1 EILDV 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-FEB-1991;
                                                                                                                                                                                                                                                                         4 BILDV
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                                                                                Sequence
                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                             RESULT 72
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RESULT 73

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which is used in an example from the present invention. The present invention describes a chimeric adenovirus fibre protein (AFP) contraining a constrained non-native amino acid sequence. The non-native amino acid sequence. The non-native amino acid sequence allows the chimeric fibre (or a vector comprising the chimeric fibre) to more efficiently bind to and enter cells. The products can be used for gene therapy, for treating cancer, e.g. melanoma, glioma and lung cancers as well as genetic disorders, e.g. cystic fibrosis, haemophilia and muscular dystrophy as well as pathogenic infections, e.g. HIV, tuberculosis and hepatitis and also for heart disease, to e.g. prevent restenosis following angioplasty or to promote angiogenesis to reperfuse necrotic tissue, and in autoimmune disorders, e.g. Crohn's disease, colitis, rheumatoid arthritis, and Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents an alpha4 integrins targeting sequence, which is used in an example from the properties of the second sequence.
                                                                             Chimeric; adenovirus; fiber protein; binding; targeting; coat protein; constrained peptide motif; gene therapy; cancer; heart disease; autoimmune disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric adenovirus fibre proteins - containing non-native amino acid sequence to provide for binding and entry into cells, especially for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 23; DB 19; Length 21; Pred. No. 71;
                                            Alpha4 integrins targeting sequence SEQ ID NO:57.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kovesdi I, Roelvink PW, Wickham TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 8; Page 57; 124pp; English.
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ilarity 100.0%;
Conservative 0;
                                                                                                                                                                                                                                                                                                                      97WO-US14719.
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  29-JUL-1998 (first entry)
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                          (GENV-) GENVEC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 AA;
                                                                                                                                                                     Synthetic.
Mastadenovirus.
                                                                                                                                                                                                                                                                                                                                                                21-AUG-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a specifically claimed non-native amino acid sequence from a chimeric adenovirus fibre protein (AFP) of the present invention. The non-native amino acid sequence allows the chimeric fibre (or a vector comprising the chimeric fibre) to more efficiently bind to and enter cells. The products can be used for gene therapy. For trearing cancer, e.g. melanoma, glioma and lung cancers as well as genetic disorders, e.g. cystic fibrosis, haemophilia and muscular dystrophy as well as pathogenic infections, e.g. HIV, tuberculosis and hepatitis and also for heart disease, to e.g. prevent restenosis following angioplasty or to promote angiogenesis to reperfuse necrotic tissue, and in autofimmune disorders, e.g. Crohn's disease, colitis, rheumatoid arthritis, and Alzheimer's disease.
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                                                                                                                                                                                                                                                                            Chimeric adenovirus fiber protein non-native amino acid sequence 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric adenovirus fibre proteins - containing non-native amino acid sequence to provide for binding and entry into cells, especially for gene therapy
                                                                                                                                                                                                                                                                                                             Chimeric; adenovirus; fiber protein; binding; targeting; coat E constrained peptide motif; gene therapy; cancer; heart disease; autoimmune disorder.
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                                                                                                                                               AAW56047 standard; peptide; 21 AA.
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                                                                                                                                                                                                                                  (first entry)
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| EILDV 9
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EILDV
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                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
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RESULT 74

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The invention provides immunogenic conjugated polypeptides which comprise a herpes simplex virus peptide (HSV) linked to an immunomodulatory peptide and which promote binding to T cells. The novel immunogenic conjugated polypeptides are effective as an immunogen in a vaccine for treatment or prevention of infection by HSV and are represented by the formula Pl-x-P2 or P2-x-P1; where Pl = a HSV specific antigenic peptide form a protein of HSV type lo or type 2, selected from ICP27, glycoprotein E. ribonucleotide reductase, ICP4, ICP34-S, glycoprotein B and CC glycoprotein F; P2 = an immunomodulatory peptide which is a portion of an immunoprotein which promotes binding to a class of subclass of T cells and which directs a predominantly TH1 type immune response to the peptide CP is and a covalent bond or a clasavable or non-cleavable peptide CP in and x = a covalent bond or a cleavable or non-cleavable peptide CP in an urmula group. The conjugated polypeptides can elicit an immune response for neuralizing HSV and killing HSV infected cells. They can be used for the polypeptide can be used for genetic immunization. They can also be the presence of infection, active or latent, in an individual by HSV by mixing T cells from the individual with the polypeptide and detecting a reaction between the T cells and the CSC polypeptide.
                                                                                                                                                                                                                                                                                                           New immunogenic conjugated polypeptides
                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 33; 69pp; English.
                                                                                                                                                             CEL-SCI CORP.
UNIV NORTHEASTERN OHIO.
                                                                                                                                                                                                                           Rosenthal KS, Zimmerman DH;
                                                                               98WO-US20681.
                                                                                                                      97US-0060422
                                                                                                                                                                                                                                                                  WPI; 1999-312418/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 AA;
WO9916710-A1.
                                                                                                                    30-SEP-1997;
                                                                               29-SEP-1998;
                                      08-APR-1999.
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                                                                                                                                                             (CELS-)
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SQ Sequence 23 AA;
Query Match
Query Matches 100.0%; Score 23; DB 20; Length 23;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels
Qy 1 EILDV 5

0; Gaps

Db 5 EILDV 9

Search completed: February 8, 2003, 10:23:45 Job time : 38 secs

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Sequence 6, Appli
Sequence 3, Appli
Sequence 6, Appli
Sequence 56, Appl
Sequence 95, Appl
Sequence 95, Appl
Sequence 95, Appl
Sequence 13, Appl
Sequence 57, Appl
Sequence 119, Appl
Sequence 119, Appl
Sequence 76, Appl
Sequence 76, Appl
Sequence 76, Appl
Sequence 900, Appl
Sequence 900, Appl
Sequence 1094, Appl
Sequence 1095, Appl
Sequence 1095, Appl
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                                                                                               ; Search time 11 Seconds
(without alignments)
10.077 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/USO8 NEW PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/NEW PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/NEW PUB.pep:*
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14: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-925-301-900
US-09-738-626-5384
US-09-738-626-4085
US-09-138-626-4085
US-09-815-242-10394
US-09-815-242-13921
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US-09-320-907B-3

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US-10-086-217-5

US-09-969-192-80

US-10-137-435-14

US-09-840-277-95

US-09-840-277-95

US-09-840-277-133

US-09-840-277-133

US-09-840-277-133

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US-09-840-277-133
                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                    129505 seqs, 22169297 residues
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                                                                                                 8, 2003, 10:24:48
                                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Sequence 14, Appl
Sequence 700, App
Sequence 6113, Ap
Sequence 492, App
Sequence 6019, Ap
Sequence 23, Appl
Sequence 23, Appl
Sequence 9, Appli
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                                                                                                                                                                                                                                                                                          Sequence 6, Application US/10086217
Sequence 6, Application US/10086217
Fatent No. US20020159998A1
GENERAL INFORMATION:
APPLICANT: WONEDA, TOSHIYUKI
TITLE OF INVENTION: METHODS OF TREATING MULTIPLE MYELOMA AND
TITLE OF INVENTION: MYELOMA-INDUCED BONE RESORPTION USING INTEGRIN
TITLE OF INVENTION: MYELOMA-INDUCED BONE RESORPTION USING INTEGRIN
TITLE OF INVENTION: MYELOMA-INDUCED BONE RESORPTION USING INTEGRIN
TITLE OF INVENTION: MYRAGEN: 2002-06-21
CURRENT PRILOR DATE: 2002-06-21
FRIOR PELICATION NUMBER: 09/943,659
FRIOR PELICATION NUMBER: 09/943,659
FRIOR APPLICATION NUMBER: 09/943,659
FRIOR APPLICATION NUMBER: 06/100,182
FRIOR PELING DATE: 2001-03-13
FRIOR PELING DATE: 1998-09-14
NUMBER OF SEQ ID NUMBER: 60/100,182
FRIOR FILING DATE: 1998-09-14
NUMBER OF SEQ ID NOS:
SEQ ID NOS:
LENGTH: S
TYPE: FRI TATESTER SET APPLICATION OF SERVICE SEQ ID NOS:
SEQ ID NOS:
TYPE: FRI TATESTER SET APPLICATION OF SERVICE SEQ ID NOS:
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TYPE: FRI TATESTER SET APPLICATION OF SERVICE SEQ ID NOS:
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; Sequence 3, Application US/09320907B
; Publication No. USZ002019836A1
; GENERAL INFORMATION:
APPLICANT: GINSBERG, MARK H.
; APPLICANT: GINSBERG, MARK H.
; TITLE OF INVENTION: TRANSMEMBRANE RECEPTORS
; TITLE OF INVENTION: TRANSMEMBRANE RECEPTORS
; TITLE REFERENCE: SRI-0006
; CURRENT FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: 09/187,236
; PRIOR APPLICATION NUMBER: 1999-11-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3; SEQ ID NO 5: 25
; LENGTH: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-10-086-217-6
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2 US-10-029-654-14

0 US-09-925-102-700

US-09-718-626-6313

0 US-09-841-132-492

US-09-738-626-6019

0 US-09-815-242-13699

US-08-910-145-014-23

US-08-910-386A-5
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     889595958
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Best Local Similarity 100.0
Matches 5; Conservative
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                                                       ; OTHER INFORMATION: Description of Artificial Sequence:Synthetic US-09-320-907B-3
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/969,192
FILING DATE: 01-Oct-2001
PRIOR APPLICATION NUMBER: US 9-455061
FILING DATE: 06-DEC-199
APPLICATION NUMBER: US 9-130225
FILING DATE: 06-AUG-1996
APPLICATION NUMBER: US 9-130225
FILING DATE: 21-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 7;
                                                                                                                100.0%; Score 23; DB 9; Length 5; 100.0%; Pred. No. 1.1e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                 Sequence 80, Application US/09969192
Patent No. US20020151027A1
GENERAL INFORMATION:
APPLICANT: WICKHAM, THOMAS J.
ROELVINK, PETRUS W.
KOVESDI, IMRE
TITLE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza - 49th Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 23; DB 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 5; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 213564
INFORMATION FOR SEQ ID NO: 80:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 80: US-09-969-192-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Hefner, M. Daniel
REGISTRATION NUMBER: 41,826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                              Query Match
Best Local Similarity 100..
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                                                                                                                                                                                                1 EILDV 5
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                                      FEATURE:
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US-10-086-217-5

RESULT

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Sequence, Non-Lication 18/10086217

FREEZAL INFORMATION:
APPLICANT: NUMBAY, GREEORY R.
APPLICANT: NUMBAY, GREEORY R.
APPLICANT: NUMBAY, GREEORY R.
APPLICANT: NUMBAY, GREEORY R.
TITLE OF INVESTION: METHODS OF REALING MULTIPLE WYELCOMA AND TITLE OF INVESTION UNESTHER SERVENCE: 0.002-06-21
CURRENT PELING WITH: 2001-06-21
CURRENT FILING NEE: 2002-06-21
FRIOR FILING NEE: 2001-06-31
FRIOR FILING NEE: 2001-06-31
FRIOR FILING NEE: 2001-06-31
FRIOR FILING NEE: 2001-06-31
FRIOR FILING NEE: 2001-06-31
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                                                                       APPLICANT: KORNO, TADAHIKO
APPLICANT: KORNO, TADAHIKO
APPLICANT: LACEY, DAVID LEE
APPLICANT: LACEY, DAVID LEE
APPLICANT: LACEY, DAVID LEE
TITLE OF INVENTION: INTEGRIN/ADHESION ANTAGONISTS
FILE REFERENCE: A-688A
CURRENT APPLICATION UNMERR: US/09/840,277
CURRENT APPLICATION NUMBER: 60/198,919
PRIOR FILING DATE: 2000-04-21
PRIOR FILING DATE: 2000-06-03
NUMBER OF SEQ ID NOS: 135
SOFTWARE: PATENTIN VEYSION 3.1
SEQ ID NO 95
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: INTEGRIN/ADHESION ANTAGONISTS FILE REFERENCE: A-688A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/840,277
CURRENT FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: 60/198,919
PRIOR FILING DATE: 2000-04-21
PRIOR APPLICATION NUMBER: 60/201,394
PRIOR FILING DATE: 2000-05-03
NUMBER OF SEQ ID NOS: 135
SOFTWARE: Patentin version 3.1
SEQ ID NO 96
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                          ; FEATURE:
; OTHER INFORMATION: Laminin related peptide
US-09-840-277-95
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; OTHER INFORMATION: Laminin related peptide
US-09-840-277-96
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Application US/09840277
320020168363A1
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Sequence 96, Application US/09840277

Patent No. US20020168363A1

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: FEIGE, ULRICH
APPLICANT: KOHNO, TADAHIKO
APPLICANT: LACEY, DAVID LEE
APPLICANT: BOONE, THOMAS CHARLES
                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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US-09-840-277-133
Sequence 95,
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/137,435
FILING DATE: 03-May-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/424,656;
FILING DATE: -UNKNOWN SP11115.7
FILING DATE: 29-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 23; DB 9; Length 12; Best Local Similarity 100.0%; Pred. No. 4.6; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                               100.0%; Score 23; DB 10; 100.0%; Pred. No. 1.1e+05;
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STREET: c/o Institute of Child Health,
30 Guildford Street
                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
                                      REFERENCE/DOCKET NUMBER: 213564
                                                                                                                      STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-09-969-192-56
NAME: Hefner, M. Daniel
REGISTRATION NUMBER: 41,826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Hart, Stephen Lewis
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: G.B.
ZIP: WCIN 1EH
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: <Unknown>
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LENGTH: 12 amino acids
                                                      INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 16
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Best Local Similarity
Matches 5; Conserva
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US-09-840-277-95
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; Pred. No. 8.5;
0; Mismatches 0; Indels
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COUNTRY: USA
ZUP: 60601
ZUP: 60601
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/969,192
FILING DATE: 01-Oct-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 59, Application US/09969192
Patent No. US20020121027A1
GENERAL INFORMATION:
APPLICANT: WICKHAM, THOMAS J.
ROBLVINK, PETRUS W.
KOVEGI, INKE
TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSES: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza - 49th Floor
CITY: Chicago
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 5; Conservative 0; Mismatches 0;
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FILING DATE: 06-DEC-1999
APPLICATION NUMBER: US 9-130225
FILING DATE: 06-AUG-1998
APPLICATION NUMBER: US 8-701124
FILING DATE: 21-AUG-1996
               STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-09-969-192-57
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REGISTRATION NUMBER: 41,826
REFERENCE/DOCKET NUMBER: 213564
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 59: US-09-969-192-59
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      amino acid
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Best Local Similarity 100.
Matches 5, Conservative
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US-09-840-277-119
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Patent No. US20020151027A1
GENERAL INFORMATION:
APPLICANT: WICKHAM, THOMAS J.
ROBLVINK, PETRUS W.
KOVESDI, IMRE
TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF CONSTRAINED PEPTIDE MOTIFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza - 49th Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                               TITLE OF INVENTION: INTEGRIN/ADHESION ANTAGONISTS
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APPLICATION NUMBER: US/09/969,192
FILING DATE: 01-0ct-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
; OTHER INFORMATION: Laminin related peptide
US-09-840-277-133
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FILING DATE: 06-DEC-1999
APPLICATION NUMBER: US 9-130225
FILING DATE: 06-AUG-1998
APPLICATION NUMBER: US 8-701124
FILING DATE: 21-AUG-1996
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NAME: Hefner, M. Daniel
REGISTRATION NUMBER: 41,826
REFERENCE/DOCKET NUMBER: 213564
                                                                                                                                                 FILE REFERENCE: A-688A
CURRENT APPLICATION NUMBER: US/09/840,277
CURRENT FILING DATE: 2001-09-14
                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/198,919
PRIOR PILING DATE: 2001-08-14
PRIOR FILING DATE: 2000-04-21
PRIOR PLING DATE: 2000-05-05
PRIOR PLING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 135
SOFTWARE: Patentin version 3:1
LENGTH: 19
                                                              KOHNO, TADAHIKO
LACEY, DAVID LEE
BOONE, THOMAS CHARLES
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 5; Conservative
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Patent No. US20020168363A1
GENERAL INFORMATION:
                                            ULRICH
                                          APPLICANT: FEIGE,
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| Patent No. US20020052308A1
| Patent No. US20020052308A1
| GENERAL INPORMATION:
| PAPLICANT: Rosen et al.
| TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
| FILE REFERENCE: PA106
| FILE REFERENCE: PA106
| CURRENT PAPLICATION NUMBER: US/09/925,301
| CURRENT FILING DATE: 2001-08-10
| PRIOR APPLICATION NUMBER: PCT/US00/05882
| PRIOR PILING DATE: 1999-03-12
| PRIOR FILING DATE: 1999-03-12
| NUMBER OF SEQ ID NOS: 1694
| SOFTWARE: PatentIN Ver. 2.0
| SEQ ID NO 900
| LENGTH: 152
| TYPE: PRT
| GRANISM: Homo sapiens
| US-09-925-301-900
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                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/969,192
FILING DATE: 01-Oct-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                       NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
STREET: Two Prudential Plaza - 49th Floor
CITY: Chicago
STATE: 111inois
COUNTRY: USA
  CONSTRAINED PEPTIDE MOTIFS
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100.0%; Score 23; DB 10;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION UNBER: US 9-455061
FILING DATE: 06-DEC-1999
APPLICATION NUMBER: US 9-130225
FILING DATE: 06-AUG-1998
APPLICATION NUMBER: US 8-701124
FILING DATE: 21-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 76:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Hefner, M. Daniel
REGISTRATION NUMBER: 41,826
REFERENCE/DOCKET NUMBER: 213564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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APPLICANT: Furcht, Leo T.
APPLICANT: Furcht, Leo T.
APPLICANT: Idea, Joji
TITLE OF INVENTION: POLYPEPTIDES WITH ALPHA 4 INTEGRIN SUBUNIT RELATED
TITLE OF INVENTION: ACTIVITY
FILE REPRENCE: 600.3320301
CURRENT APPLICATION NUMBER: US/09/010,714
CURRENT PILING DATE: 1998-01-22
SOFTWARE: PALEGALIN Ver. 2.0
SEQ ID NO 11
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10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 23; DB 9; Length 25; 100.0%; Pred. No. 10; tive 0; Mismatches 0; Indels
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Patent No. US20020151027A1
GENERAL INPORMATION:
APPLICANT: WICKHAM, THOMAS J.
ROGILVINK, PETRUS W.
KOVESDI, IMRE
TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                    TITLE OF INVENTION: INTERINA ANTAGONISTS
FILE REFERENCE: A-688A
CURRENT APPLICATION NUMBER: US/09/840,277
CURRENT APPLICATION NUMBER: 06/198,919
PRIOR APPLICATION NUMBER: 60/198,919
PRIOR RILING DATE: 2000-04-21
PRIOR APPLICATION NUMBER: 60/201,394
PRIOR FILING DATE: 2000-05-03
NUMBER OF SEQ ID NOS: 135
SOFTWARE: PATENTIN OFFISION 3.1
SEQ ID NO 119
LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Laminin related peptide US-09-840-277-119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 23; 100.0%; Pred. No. 1
Sequence 119, Application US/09840277 Patent No. US20020168363A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11, Application US/09010714
Patent No. US20020012942A1
GENERAL INFORMATION:
                                                                    APPLICANT: FRIGR, ULRICH
APPLICANT: KOHNO, TADALHIKO
APPLICANT: LACEY, DAVID LEE
APPLICANT: BOONE, THOMAS CHARLES
                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-010-714-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
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US-09-969-192-76
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US-09-010-714-11
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                                                                                                                                                                         Query Match 100.0%; Score 23; DB 9; Length 344; Best Local Similarity 100.0%; Pred. No. 1.8e+02; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Oblsen, Kari L.
APPLICANT: Oblsen, Kari L.
APPLICANT: Oblsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yanamoto, Robert T.
APPLICANT: Yanamoto, Robert T.
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APPLICANT: Yanamoto, Robert T.
APPLICANT: Yanamoto, Robert T.
APPLICANT: Yanamoto, Robert T.
PRIOR PILING DATE: 2000-05-28
PRIOR PILING DATE: 2000-10-22
PRIOR APPLICATION NUMBER: 60/283,625
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
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PRIOR FILING DATE: 2000-11-27
PRIOR PORTICATION NUMBER: 60/269, 308
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10394, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Chisen, Kari L.
APPLICANT: Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13921, Application US/09815242
Patent No. US20020061569A1
GENEAL-INPORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Systind, Judith W.
APPLICANT: Wall, Daniel
                                                         ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Escherichia coli
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286 EILDV 290
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US-09-815-242-10394
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US-09-815-242-13921
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SEQ ID NO 4085
LENGTH: 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: TYKOI, HARUHIKO
APPLICANT: TEKDA, MANOKO
APPLICANT: TEKDA, MASATO
APPLICANT: TEKDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: ANDO, SEIKO
APPLICANT: OCHIAI, KEIKO
APPLICANT: OCHIAI, KEIKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: TATEISHI, NAOKO
APPLICANT: IKEDA, MASATO
APPLICANT: AKIO
APPLICANT: AKIO
TITLE OF INVEWTION: NOVEL POLYNUCLEOTIDES
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CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR PILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR APPLICATION NUMBER: UP 00/280988
PRIOR FILING DATE: 2000-04-07
PRIOR PELING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
                                                                                                             RESULT 16
US-09-738-626-5384
US-09-738-626-5384
Sequence 5384, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-738-626-4085

Sequence 4085, Application US/09738626

Publication No. US20020197605A1

GENERAL INFORMATION:

APPLICANT: NAKAGAWA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT Orynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 5; Conservative
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12 EILDV 16
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GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION:

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/09/925,302

CURRENT APPLICATION NUMBER: DCT/US00/05918

PRIOR APPLICATION NUMBER: PCT/US00/05918

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR FILING DATE: 1999-03-12

NUMBER: OF SEQ ID NOS: 896

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 700
                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 100.0%; Score 23; DB 10; Length 417; Best Local Similarity 100.0%; Pred. No. 2.2e+02; Matches 5; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AFFLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR PILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR APPLICATION NUMBER: UP 00/280988
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: UP 00/280988
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
SOFTWARE: PATENTIN VOY: 3.0
SEQ ID NO 6313
LENGTH: 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6313, Application US/09738626
Sequence 6313, Application US/09738626
GENERAL INFORMATION:
APPLICANT: MAKAGAMA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SBIKO
APPLICANT: HAYASHI, MIKIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100...
S. Conservative
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IKEDA, MASATO
OZAKI, AKIO
    Patent No. US20020044941A1
                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-09-925-302-700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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Fatent No. US20020150958A1
GENERAL INFORMATION:
APPLICANT: Boehringer Ingelheim Pharma KG
TITLE OF INVENTION:
TITLE OF INVENTION: inflammatory conditions,
FILE REFERENCE: 1/178 B4
CURRENT APPLICATION NUMBER: US/10/029,654
CURRENT FILING DATE: 2001-12-21
FRIOR APPLICATION NUMBER: US 60/257,878
FROM FILING DATE: 2000-12-22
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
LENGTH: 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 23; DB 10; Length 366; 100.0%; Pred. No. 1.9e+02; Live 0; Mismatches 0; Indels (
           APPLICANT: TIMILE, Grant J.
APPLICANT: Cart. Grant J.
APPLICANT: Cart. Grant J.
APPLICANT: Yamamoco, Robert T.
APPLICANT: Yamamoco, Robert T.
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
FILE REPERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PESESEQ FOR WINDOWS VERSION 4.0
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Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Salmonella typhi
US-09-815-242-13921
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Best Local Similarity 100.
Matches 5; Conservative
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Matches 5; Conservative
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; ORGANISM: Homo sapiens
US-10-029-654-14
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US-09-925-302-700
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US-10-029-654-14
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535 EILDV 539
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; Patent No. US20020061848A1
; GENERAL INFORMATION:
; APPLICANT: Bhatis, Yasir A.W.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Probet, Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.46908
; CURRENT APPLICATION NUMBER OF SEQ 10 NOS: 599
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 492
; LENGTH: 560
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100.0%; Score 23; DB 10; Length 560;

Best Local Similarity 100.0%; Pred. No. 3.1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels (
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100.0%; Score 23; DB 9; Length 706;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
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TILLE OLIVENTION: NOVEL POLYNUCLEOTIDES
FILLE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SEQ ID NO 6019
LENGTH: 706
                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: VARIANT
COCATION: (1)...(560)
COTHER INFORMATION: Xaa = Any Amino Acid
WS-09-841-132-492
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; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6019, Application US/09738626
Publication No. US20020197605A1
BEREAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
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ANDO, SEIKO
HAYASHI, MIKIRO
OCHIALI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
OZAKI, AKIO
                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Chlamydia pneumoniae
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Sequence lighs, Application US/09815242

Packer No. US20000061569A.

Packer No. US20000061569A.

APPLICANT Massibock, Robert
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PRIOR FILING DARE: 2000-03-21

PRIOR PILING DARE: 2000-03-22

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PRIOR PILING DARE: 2000-03-22

PRIOR PILING DARE: 2000-03-23

PRIOR PILING DARE: 2000-03-23

PRIOR PILING DARE: 2000-03-24

APPLICANT: TRAIN DARE: 1938

DARESTOR PILING DARE: 2000-03-14

APPLICANT: TRAIN DARE: 1938

DARESTOR TRAINSTORM DARE: 1938

PRIOR PILING DARE: 1930-03-14

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APPLICANT: TRAIN DARE: 1938

PRIOR PILING DARE: 1930-03-14

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GENERAL INFORMATION
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Sequence 9, Application US/08910386A

Sequence 9, Application US/08910386A

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Sequence 9, Application US/08910386A

SEQUENCE OF US/0802041A1

SEQUENCE OF US/0802041A1

SEQUENCE OF US/08041A1

SEQUENCE OF US/08041A1

SEQUENCE OF US/08041A1

SEQUENCE OF SEQUENCES: 53

CORRESPONDENCE ADDRESS: 53

CORRESPONDENCE ADDRESS: 53

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California
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100.0%; Pred. No. 4.70+02;
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MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentun Release #1.0, Version #1.30

SOFTWARE: Patentun Release #1.0, Version #1.30

SOFTWARE: Patentun Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/08/910,386A

FILING DATE: 13-AUG-1997

CLASSIFICATION: NUMBER: US/08/910,386A

FRICTATION NUMBER: 03.070-058950US

FREISPACHION INFORMATION:

REGISTRATION NUMBER: 03.070-058950US

TELEPHONE: (415) 576-0300

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 813 amino acids

TYPE: amino acid

TOPOLOGY: Inear

MOLECULE TYPE: protein

US-08-910-386A-9
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100.0%; Score 23; DB 9; I
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 0;
SOFTWARE: PatentIn version 3.1 SEQ ID NO 23 LENGTH: 784
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Best Local Similarity 100.
Matches 5; Conservative
                                                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-145-014-23
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; Sequence 5, Application US/08910386A ; Patent No. US20020092041A1

RESULT 28 US-08-910-386A-5

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### APPLICANT: Ronad, pamera C.
### APPLICANT: Song, Wen-Yuang
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US-08-467-580-3
US-09-130-225-56
US-09-025-622-3
                                                                                                                                                                                                                                                                                                                             262574 segs, 29422922 residues
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                 GenCore version (c) 1993 - 2003
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Maximum Match 100%
Listing first 100 summaries
                                                                                                                         2003, 10:23:08
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Perfect score:
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Maximum DB R
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RESULT 1

US-06-10-106-3

SQUENCE 3, Application US/08109106

FREEDER NO. 5475100

FRIEDER PROPERTION: HERSHING Et al.

TITLE OF INVESTION: Wendercot, Lind & Ponack

STREET: No. 5175100

STREET: SOS FIffeenth Street, N.W., #700

STREET: SOS FIffeenth Street, N.W., #700

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100.0%; Score 23; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                        Length 5;
                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1.2. Application US/08303162A

Patent No. 555909

GENERAL INFORMATION:
APPLICANT: Wickham, Thomas J.
APPLICANT: Wickham, Time
APPLICANT: Brough, Douglas E.
APPLICANT: McVey, Duncan L.
APPLICANT: McVey, Duncan L.
TITLE OF INVENTION: CHIMERIC PENTON BASE MOLECULES
TITLE OF INVENTION: AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 60601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,162A
                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 23; DB 1; I
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0;
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FILLING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kilyk, John Jr.
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 61306
TELECHOMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
TELEPHONE: (312) 616-5700
TELEFAX: (312) 616-5700
SINPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
**FANGTH: 5 amino acids
               TITLE:

JOURNAL:

JOURNAL:

JOSUB:

PACES:

DOCUMENT NUMBER:

FILING DATE:

FILING DATE:

RELEVANT RESIDUES IN SEQ ID NO:

US-08-109-106-3
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MOLECULE TYPE: protein
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STRANDEDNESS: single
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AUTHORS:
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                                                                                                                                                                                                                FILING DATE:
PRICE APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION WUMBER: 07/814,873
FILING DATE: December 24, 1991
PRIOR APPLICATION DATA:
APPLICATION WUMBER: 07/402,389
FILING DATE: September 1, 1989
ATTORNEY, AGENT INFORMATION:
NAME: SUNGMEN, JOHN, S.
REGISTRATION NUMBER: 34,446
REFERENCE/DOCKET NUMBER: 34,446
REFERENCE/DOCKET NUMBER: CYTE-1-6162
TELECOMMUNICATION INFORMATION:
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APPLICANT: Kovesdi, Imre
APPLICANT: Kovesdi, Imre
APPLICANT: Brough, Douglas B.
APPLICANT: Broden, Douglas B.
APPLICANT: Bruder, Joseph T.
TITLE OF INVENTION: CHIMERIC PENTON BASE MOLECULES
TITLE OF INVENTION: AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS: 24
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 98101-2347
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage COMPUTER: IBM PC/386 Compatible OPERATING SYSTEM: MS-DOS 4.01 SOFTWARE: Word for Windows-t CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338,282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,515
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/303,162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-709-515-3
; Sequence 3, Application US/08709515
; Patent No. 5731190
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 1-206-224-0779
TELEX: 4938023
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 5 amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
DESCRIPTION:
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Sequence 3, Application US/08634060

Sequence 3, Application US/08634060

Patent No. 5712136

Patent No. 5712136

Patent Koveedi, Imre

APPLICANT: Wickham, Thomas J.

APPLICANT: Koveedi, Imre

APPLICANT: Roelvink, Petrus W.

TITLE OF INVENTION: THE ADENOVIRAL-MEDIATED CELL TARGETING COMMANDED BY

TITLE OF INVENTION: THE ADENOVIRUS PENTON BASE PROTEIN

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSEE: Leydig, Voit & Mayer, Ltd.
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CURRENT APPLICATION DATA:
CUBLICATION NUMBER: US/08/634,060
FILING DATE:
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100.0%; Pred. No. 1.9e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                  B: Leydig, Voit & Mayer, Ltd. Two Prudential Plaza, Suite 4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIPCATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/303,162
FILING DATE: 08-SEP-1994
CLASSIFICATION: 514
ATTONEY/AGANT INFORMATION:
NAME: KILYK, John Jr.
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 71602
TELEPHONE: (312) 616-5600
TELEPHONE: (312) 616-5600
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 100.
Matches 5; Conservative
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STRANDEDNESS: single
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MOLECULE TYPE: protein

US-08-634-060-3
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STATE: Illinois
COUNTRY: USA
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                                                                                                                                                                                                                    APPLICANT: Jeffrey W. Smith
APPLICANT: Jeffrey W. Smith
TITLE OF INVENTION: Integrin Ligand Dissociators
FILE REPERRICE: 02046.0002
CURRENT APPLICATION NUMBER: US/09/146,503
CURRENT FILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: 60/057,463
EARLIER FILING DATE: 1997-09-03
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO: 3
LENGTH: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Synthetically generated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 23; DB 4;
100.0%; Pred. No. 1.9e+05;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Cast.O. ALIENGED C.
APPLICANT: Cuervo, Julio Herman
APPLICANT: Lee, Wen-Cherng
APPLICANT: Lee, Wen-Cherng
APPLICANT: Lee, Wen-Cherng
APPLICANT: Carter, Mary Beth
APPLICANT: Almquist, Ronald G.
APPLICANT: Almquist, Ronald G.
APPLICANT: Almquist, Ronald G.
APPLICANT: Almquist, Ronald G.
APPLICANT: Almquist, Ronald G.
APPLICANT: Disinger, Carol Lee
TITLE REFERENCE: 10274/02402
CURRENT APPLICATION NUMBER: US/08/983,391
CURRENT FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: US 96/11570
PRIOR APPLICATION NUMBER: US 08/498,237
PRIOR APPLICATION NUMBER: US 08/498,237
PRIOR APPLICATION NUMBER: US 08/498,237
SOFTWARE: PASESEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 5
                                                                                                                                                        Sequence 3, Application US/09146503
Patent No. 6184206
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08983391
Patent No. 6239108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence

// OTHER INFORMATION: Synthetic
US-09-146-503-3
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Adams, Steven P.
Castro, Alfredo C.
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Best Local Similarity 100.0
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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        EILDV
                                                                                                                                    US-09-146-503-3
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                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | Sequence 2, Application US/08700846
| Patent No. 5962311
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: WICKHAM, THOMAS J.
| APPLICANT: KOVESDI, IMRE
| TITLE OF INVENTION: A SHORT-SHAFTED ADENOVIRAL FIBER AND ITS
| TITLE OF INVENTION: USE
| NUMBER OF SEQUENCES: 17
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: LEYDIG, VOIT & MAYER, LTD.
| STREET: TWO PRUDENTIAL PLAZA, SUITE 4900
| CITY: CHICAGO
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                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: CALLACY
COUNTRY: USA
ZIP: 60601-6780

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Pacentin Release #1.0, Version #1.25
SOFTWARE: Pacentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,846
FLING DATE: 21-AUG-1996
CLASSIFICATION: 51
ATTORNEY/AGENT INFORMATION:
NAME: LARCHER, CAROL
REGISTRATION NUMBER: 35243
REFERENCE/DOCKET NUMBER: 35243
TELECOMMUNICATION INDER: 35043
FILING DATE: 08-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: KILYK, JOHN Jr.
REGISTRATION NUMBER: 30763
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
TELEFAX: (312) 616-5700
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
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TELEFAX: (312) 616-5700
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                    TOPOLOGY: linear; MOLECULE TYPE: protein US-08-709-515-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
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                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIONS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/376,372
FILING DATE:
FLING DATE:
FLING DATE:
FRIENCE/CONTRACTION:
NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: 27,794
REFERENCE/DOCKET NUMBER: 27,794
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SOF.9000
TELECCOMMUNICATION FOR SOF.9000
TELECCOMMUNICATION FOR SOF.9000
TELECCOMMUNICATION FOR SOF.9000
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Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0;
APPLICANT: Castro, Alfredo C
APPLICANT: Zimmerman, Craig N
APPLICANT: Hammond, Charles E
APPLICANT: Liao, Yu-Sheng
TITLE OF INVENTION: CELL ADHESION INHIBITORS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lin, Ko-Chung
APPLICANT: Lin, Ko-Chung
APPLICANT: Lin, Ko-Chung
APPLICANT: Lew Wen-Cherng
APPLICANT: Castro, Alfredo C.
APPLICANT: Zimmerman, Craig N.
APPLICANT: Liao, Yu-Sheng
APPLICANT: Liao, Yu-Sheng
APPLICANT: Liao, Yu-Sheng
APPLICANT: Liao, Yu-Sheng
APPLICANT: Liao, Yu-Sheng
APPLICANT: Liao, Yu-Sheng
APPLICANT: Liao, Yu-Sheng
APPLICANT: Liao, Yu-Sheng
APPLICANT: Liao, Yu-Sheng
APPLICANT: Singh, Juswinder
ITLE REFERENCE: 10274-023002
CURRENT APPLICATION NUMBER: US/08/875,321
CURRENT APPLICATION NUMBER: US 08/376, 372
PRIOR APPLICATION NUMBER: US 08/376, 372
PRIOR APPLICATION NUMBER: US 08/376, 372
PRIOR APPLICATION NUMBER: US 08/376, 372
PRIOR APPLICATION NUMBER: US 08/376, 372
PRIOR PILING DATE: 1995-01-23
NUMBER OF SEQ ID NOS: 5
SEQ ID NO 2
LENGTH: S
                                                                                                                                                                                                                                                                                                                                                                     New York
: United States of America
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Patent No. 6376538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                              STATE: New
COUNTRY: Un
ZIP: 10020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EILDV 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lee, Wen-Cherng
APPLICANT: Lee, Wen-Cherng
APPLICANT: Lee, Wen-Cherng
APPLICANT: Carter, Mary B
APPLICANT: Carter, Mary B
APPLICANT: Carter, Mary B
APPLICANT: Carter, Mary B
APPLICANT: Carter, Mary B
APPLICANT: Almquist, Ronald G
TITLE OF INVENTION: CELL ADHESION INHIBITORS
NUMBER OP SEQUENCES:
ADDRESSE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/498,237
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                           RESULT.
US-08-498-237-2
Sequence 2, Application US/08498237
Fatent No. 6548713
GENERAL INFORMATION:
APPLICANT: Lin, Ko-Chung
APPLICANT: Adams, Steven P
APPLICANT: Castro, Alfredo C
APPLICANT: Castro, Alfredo C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08376372
Patent No. 6306840
GENERAL INFORMATION:
APPLICANT: Adams, Steven P
APPLICANT: Lin, Ko-Chung
APPLICANT: Lin, Ko-Chung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zimmerman, Craig N
Cuervo, Julio H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-498-237-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 5; Conserv
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                                            EILDV S
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Gaps

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Sequence 50, Application US/08860248C

Patent No. 6034056

GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
PERRONECTIN ADHESION INHIBITORS
NUMBER OF SEQUENCES:
ADDRESSE:
Pillsbury Madison & Sutro, L.L.P.
STREET:
CORRESPONDENCE ADDRESS:
ADDRESSE:
PILLON NEW YORK Avenue, N.W.
CITY: Washington
STREET:
COMPUTER: D.C.
COMPUTER: D.C.
COMPUTER: TBM PC Compatible
COMPUTER: TBM PC Compatible
COMPUTER: TBM PC Compatible
COMPUTER: TBM PC Compatible
COMPUTER: TBM PC COMPATIBLE
COMPUTER: TBM PC COMPATIBLE
COMPUTER: ADDRESS:
MEDIUM TYPE: TBM PC COMPATIBLE
COMPUTER: ADDRESS:
CLASSIFICATION NATE:
PRICATION NUMBER: GB 9426254.0
FILING DATE: 24-DBC-1994
PRICATION NUMBER: GB 9513904.4
FILING DATE: 24-DBC-1994
PRICATION NUMBER: GB 9513904.4
FILING DATE: 23-DBC-1995
FILING DATE: 23-DBC-1995
FILING DATE: 23-DBC-1995
FILING DATE: 23-DBC-1995
FILING DATE: 23-DBC-1995
FILING DATE: 23-DBC-1995
FILING DATE: 23-DBC-1995
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FILING DATE: 23-DBC-1995
FILING DATE: 33-DBC-1995
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FILING 
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/note= "3-AMINO-PROPIONIC ACID"
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/701,124
FILING DATE: 21-AUG-1996
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3;
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                                                                                                                                                                                                                                                                LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: circular MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: 7
; OTHER INFORMATION:
; OTHER INFORMATION:
US-08-860-248C-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Peptide LOCATION: 7
                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EILDV 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: STRUCTURAL MODELS FOR CYTOPLASMIC
TITLE OF INVENTION: DOMAINS OF TRANSMEMBRANE RECEPTORS
NUMBER OF SEQUENCES: 20
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07542
FILING DATE: 13-UNM-1995
PRIOR APPLICATION NUMBER: USSN 08/260,514
FILING DATE: 15-UNM-1994
INFORMATION FOR SEQ ID NO.: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                          100.0%; Score 23; DB 4; Length 5; 100.0%; Pred. No. 1.9e+05; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vuery match

Best Local Similarity 100.0%; Pred. No. 1.9e+05; Length 5; Matches 5; Conservative n. Minches
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Patent No. 5846782

GENERAL INFORMATION:

APPLICANT: Rickham, Thomas J.

APPLICANT: Roelvink, Petrus W.

ATILLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF TITLE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS

NUMBER OF SEQUENCES: 80

CORRESPONDENCE ADDRESS:

ADDRESSEE: Leydig, Voit & Mayer, Ltd.

STREET: Two Prudential Plaza - 49th Floor

CITY: Chicago

STATE: Illinois

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Ligand sequence recognized by integrin
                                                                ; OTHER INFORMATION: Synthetically generated peptide
US-08-875-321-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application PC/TUS9507542
GENERAL INFORMATION:
APPLICANT:
           ORGANISM: Artificial Sequence
                                                                                                                       Query Match
Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 amino acida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
GY: linear
                                                                                                                                                                                                                                                                                                   1 EILDV 5
                                                                                                                                                                                                                                                             1 EILDV 5
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                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
PCT-US95-07542-3
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                                        FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
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Length 7;
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Batent No. 6034056

GENERAL INFORMATION:
APPLICANT: DUTTA, Anand
TITLE OF INVENTION: FIBRONECTIN ADHESION INHIBITORS
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "OTHER"
/note= "6-AMINO-HEXANOIC ACID"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 23; DB 3; I
100.0%; Pred. No. 1.9e+05;
  B: Pillsbury Madison & Sutro, L.L.P. 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                          SOFTWARE: MS WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,248C
FILING DATE: 24-UNE-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9426254.0
FILING DATE: 24-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9505905.1
FILING DATE: 23-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9513904.4
FILING DATE: 07-JUL-1995
INFORMATION FOR SEQ ID NO: 52:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,248C
FILING DATE: 24-JUNE-1997
CLASSIPICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9426254.0
                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006-3918
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: circular
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 7
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Peptide
ADDRESSEE: Pillsk
STREET: 1100 New
CITY: Washington
                                                                                     RY: U.S.A.
20005-3918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-860-248C-52
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US-08-860-248C-53
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                        0; Indels
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                                                                                                                                                            RESULT 15
US-08-660-246C-51
Sequence 51, Application US/08860248C
Sequence 51, Application US/08860248C
Setent No. 6034056
GENERAL INFORMATION:
APPLICANT: UNTAY, Anand
TITLE OF INVENTION:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 16
US-08-860-248C-52
US-08-860-248C
; Sequence 52, Application US/08860248C
; Patent No. 6034056
; GENERAL INFORMATION:
; APPLICANT: DUTTA, Anand
; TITLE OF INVENTION: FIBRONECTIN ADHESION INHIBITORS
; NUMBER OF SEQUENCES: 122
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "5-AMINO-PENTANOIC ACID
100.0%; Pred. No. 1.9e+05;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: BM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,248C
FLING DATE: 24-UUNE-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: GB 9426254.0
FILING DATE: 24-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: GB 9505905.1
FILING DATE: 23-MAR-1995
PRIOR APPLICATION DATA:
FILING DATE: 07-UUL-1995
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
WUND: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= "OTHER"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 5; Conservative
                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: circular
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCATION: 7
CTHER INFORMATION: CTHER INFORMATION: US-08-860-248C-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Peptide
Best Local Similarity
Matches 5; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A. ZIP: 20005-3918
                                                             1 RILDV 5
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Query Match
Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 23; DB 3; Length 7; 100.0%; Pred. No. 1.9e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 23; DB 3; Length 7; 100.0%; Pred. No. 1.9e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 80, Application US/09130225
; Patent No. 6057155
; GENERAL INFORMATION:
APPLICANT: Wickham, Thomas J.
APPLICANT: Kovedi, Inre-
TILE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
TILE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza - 49th Floor
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                        /product= "OTHER"
/note= "8-AMINO-OCTANOIC ACID"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/130,225
FILING DATE: 24-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9505905.1
FILING DATE: 23-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9513904.4
FILING DATE: 07-JUL-1995
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acids
STRANBENNES: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 8-701124
FILING DATE: 21-AUG-1996
INFORMATION FOR SEQ 1D NO: 80:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                     SS: single circular
                                                                                                                                                                                                                                   TOPOLOGY: circular
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: peptide US-09-130-225-80
                                                                                                                                                                                                                                                                        FEATURE:

NAME/KEY: Peptide

LOCATION: 7

OTHER INFORMATION: //

US-08-860-248C-53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 60601
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Patent No. 522936

GENERAL INFORMATION:
APPLICANT: TSUKADA, Yoshihisa
APPLICANT: ORIKASA, Atsushi
TITLE OF INVENTION: PEPTIDE-CONTAINING POLYETHYLENE GLYCOL
TITLE OF SEQUENCES:
INVERS
Sequence 80, Application US/09455061

Patent No. 6329190

GENERAL INFORMATION: Thomas J.

APPLICANT: Roelvink, Petrus W.

APPLICANT: Kovedi, Interesting Denovirus WITH USE OF TITLE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS

TITLE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS

TITLE OF INVENTION: Voit & Mayer, Ltd.

STREET: Two Prudential Plaza - 49th Floor

CITY: Chicago

STATE: Illinois

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/455,061

FILING DATA:

APPLICATION NUMBER: US 9-130225

FILING DATE: O6-AMG-1998

PILING DATE: O6-AMG-1998

PILING DATE: 21-AMG-1996

ATTORNEY/AGENT INFORMATION:

NAME: HEFRET 1.0 NUMBER: 41,826

REGISTRATION NUMBER: 41,826

REGISTRATION NUMBER: 41,826

REFERENCE/DOCKET NUMBER: 203128

INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Sughrue, Mion, Zinn, Macpeak and Seas STREET: 2100 Pennsylvania Avenue, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 23; DB 4;
100.0%; Pred. No. 1.9e+05;
iive 0; Mismatches 0;
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Sequence 7, Application US/08338282
Patent No. 5730978
GENERAL INFORMATION:
APPLICANT: WAYNER, E.A.
TITLE OF INVENTION: INHIBITION OF LYMPHOCYTE ADHERENCE TO VASCULAR ENDOTHELIUM NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christeensen, O'Connor, Johnson and Kindness
STREET: 2800 Pacific First Center, 1420 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                         100.0%; Score 23; DB 1; Length 8; 100.0%; Pred. No. 1.9e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSES: CITISTERISED, O'CORNOI, JOHNSON AND ALGEBEE STREET: 2000 Pacific First Center, 1420 Fifth Avenue CITY: Seattle
STATE: Washington
COUWIRY: USA
ZIP: 98101-2347
COMFUTER: BASELE FORM:
MEDIOL TYPE: Diskette-5.25 inch, 1.2Mb storage
COMPUTER: Diskette-5.25 inch, 1.2Mb storage
COMPUTER: Diskette-5.25 inch, 1.2Mb storage
COMPUTER: Diskette-5.25 inch, 1.2Mb storage
COMPUTER: Diskette-5.25 inch, 1.2Mb storage
COMPUTER: Diskette-5.25 inch, 1.2Mb storage
COMPUTER: Diskette-5.25 inch, 1.2Mb storage
COMPUTER: Diskette-5.25 inch, 1.2Mb storage
COMPUTER: Diskette-5.25 inch, 1.2Mb storage
COMPUTER: Diskette-5.25 inch, 1.2Mb storage
COMPUTER: Diskette-5.25 inch, 1.2Mb storage
COMPUTER: Diskette-5.25 inch, 1.2Mb storage
COMPUTER: Diskette-5.25 inch, 1.2Mb storage
COMPUTER: Diskette-5.25 inch, 1.2Mb storage
COMPUTER: Diskette-5.25 inch, 1.2Mb storage
COMPUTER: Diskette-5.25 inch, 1.2Mb storage
COMPUTER: Diskette-5.25 inch, 1.2Mb storage
COMPUTER: Diskette-5.25 inch, 1.2Mb storage
COMPUTER: Diskette-5.25 inch, 1.2Mb storage
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COMPUTER: Diskette-5.25 inch, 1.2Mb storage
COMPUTER: Diskette-5.24-0779
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US-08-701-124-56
; Sequence 56, Application US/08701124
; Patent No. 5846782
; GENERAL INFORMATION:
                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
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DESCRIPTION:
         HYPOTHETICAL:
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                     us-08-158-936-1
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Patent No. 5521067
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Bone Marrow Cell Adhesion Molecules and
TITLE OF INVENTION: Process for Detecting Adherence Between Cell Adhesion
TITLE OF INVENTION: Molecules and Cells Generally
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS: 1
CORRESPONDENCE ADDRESS: 3
ADDRESSEE: Mixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
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STATE: New York
COUNTRY: U.S.A.

ZIP: 14603
COMPUTER READABLE FORM:
RUBLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/158,936
FILING DATE: No. 5521067ember 24, 1993 (
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCES/DOCKET NUMBER: 176/60030
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
COUNTRY: USA
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 19911021
CLASSIFICATION: 530
FELECOMMUNICATION: 530
TELECOMMUNICATION: 530
TELECOMMUNICATION: 202-293-7060
TELECAM: 4091103
TELEFRAX: 202-293-7060
TELEFRAX: 202-293-7060
TELEFRAX: SOSO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TELENTH: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Matches 5; Conservative
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-07-780-081-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
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TYPE: PRT
ORGANIDM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide
OTHER INFORMATION: derived from fibronectin
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Sequence 56, Application US/09130225

Sequence 56, Application US/09130225

GENERAL INFORMATION:

APPLICANT: Wickham, Thomas J.

APPLICANT: Roelvink, Petrus W.

APPLICANT: Rovedi, Imre PAPLICANT:

TITLE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS

TUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Leydig, Voit & Mayer, Ltd.

STREET: Two Prudential Plaza - 49th Floor
                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 23; DB 2; Length 8; Best Local Similarity 100.0%; Pred. No. 1.9e+05; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 8;
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US-08-467-580-3
IS-08-467-580-3
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Pred. No. 1.9e+05;
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Best Local Similarity 100.0%;
Matches 5; Conservative 0;
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; OTHER INFORMATION: ACETYLATION
US-08-467-580-3
                                                                                                                                                          LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: Two Prudiction CITY: Chicago STATE: Illinois COUNTRY: USA
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NAME/KEY: MOD_RES
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1 BILDV 5
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Patent No. 5558874
GENERAL INFORMATION:
APPLICANT: Clark, Richard A
APPLICANT: Gailing, Doris
APPLICANT: Gailin, James
TITLE OF INVENTION: EXCOMBINANT FIBRONECTIN-BASED
TITLE OF INVENTION: EXTRACELLULAR MATRIX FOR WOUND HEALING
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jaeckle Fleischmann & Mugel, LLP
STREET: 39 State Street
APPLICANT: Roelvink, Petrus W.
APPLICANT: Roelvink, Petrus W.
TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
TITLE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lapoping, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza - 49th Floor
CITY: Chicago
STREET: Illinois
COUNTRY: USA
ZIP: 6067.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 23; DB 2; Length 8; Best Local Similarity 100.0%; Pred. No. 1.9e+05; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Rochester STATE: New York COUNTRY: New York COUNTRY: New York COUNTRY: READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CARRENT APPLICATION DATA: APPLICATION NUMBER: US/09/025,706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Braman, Susan J
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 87653.97R263
TELEPHONE: 716-269-3640
TELEPHONE: 716-262-4133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
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US-09-025-706-3
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US-08-983-391-1
; Pred. No. 1.9e+05; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lee, Wen-Cherry
APPLICANT: Hammond, Charles E.
APPLICANT: Hammond, Charles E.
APPLICANT: Almquist, Mary Beth
APPLICANT: Almquist, Ronald G.
APPLICANT: Almquist, Ronald G.
APPLICANT: Ensinger, Carol Lee
FILLE OF INVENTION: CELL ADHESION INHIBITORS
FILE REPERENCE: 10274/02402
CURRENT APPLICATION NUMBER: US 96/11570
PRIOR APPLICATION NUMBER: US 96/11570
PRIOR PILING DATE: 1995-07-11
PRIOR FILING DATE: 1995-07-11
PRIOR FILING DATE: 1995-07-11
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FASTERY FOR WINDOWS VERSION 4.0
LENGTH: B
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APPLICANT: Hammond, Charles B
APPLICANT: Carter, Mary B
APPLICANT: Almquist, Ronald G
TITLE OF INVENTION: CELL ADHESION INHIBITORS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: United States of America ZIP: 10020
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08983391
Patent No. 6239108
GENERAL INFORMATION:
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Patent No. 6248713
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lin, Ko-Chung
Adams, Steven P.
Castro, Alfredo C.
Zimmerman, Craig N.
Cuervo, Julio Herman
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Zimmerman, Craig N
Cuervo, Julio H
100.08;
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Adams, Steven P
Best Local Similarity 100.
Matches 5; Conservative
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STATE: New York
                                                                                                                      1 RILDV S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 BILDV 5
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                                                                                                                                                                                          1 RILDV
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US-08-498-237-1
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APPLICANT:
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APPLICANT:
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| Sequence 3, Application US/09025622
| Patent No. 6194379|
| Patent No. 6194370|
| APPLICANT: Clark, Richard A APPLICANT: Clark, Richard A APPLICANT: Greiling, Doris | TITLE OF INVENTION: MATRIX FOR WOUND HEALING | NUMBER OF SEQUENCES: ADDRESSEE: Jackle Fleischmann & Mugel, LLP | STREET: 39 State Street | CITY: Rochester | CITY: Rochester | CITY: Rochester | CITY: Rochester | CITY: New York | CITY: STATE: New York | CITY: STATE: New York | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CITY: Compared | CIT
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                                      COMPUTER ALL.

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BEN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/130,225
FILING DATE: 21-AUG-1996
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids

"The Author acids and a state of the author acids and a state of the author acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids and acids acids and acids and acids and acids and acids and acids and acids and acids acids and acids and acids and acids and acids and acids and acids acids acids and acids acids acids acids and acids acids acids acids acids acids acids acids acids acids acids acids 
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CAPRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,622
FILING DATE:
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100.0%; Pred. No. 1.9e+05;
vative 0; Mismatches 0;
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NAME: Braman, Susan J
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 87653.97R270
TELEPHONE: 716-262-3640
TELEPHONE: 716-262-4133
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acid
TYPE: amino acid
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MOLECULE TYPE: peptide
US-09-130-225-56
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ZIP: 60601
COMPUTER READABLE FORM:
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APPLICANT: Roelvink, Petrus W.
APPLICANT: Rovesdi, Imre
TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
TITLE OF INVENTION: CONSTRAINED PEPTIDE WOTIFS
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/455,061

FILING DATE: 06-DEC-1999

PRIOR APPLICATION NUMBER: US 9-130225

FILING DATE: 06-AUG-1998

PRIOR APPLICATION NUMBER: US 9-701124

FILING DATE: 10-AUG-1996

ATTORNEY/AGENT INFORMATION:

NAME: Hefner, M. Daniel

REFERENCE/DOCKET NUMBER: 41,826

REFERENCE/DOCKET NUMBER: 203128

INFORMATION FOR SEQ ID NO: 56:

SEQUENCE CHARGENISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 23; DB 4; L
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                             100.0%; Score 23; DB 4; I 100.0%; Pred. No. 1.9e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza - 49th Floor
CITY: Chicago
STATE: 11linois
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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Patent No. 6329190
GENERAL INFORMATION:
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STRANDEDNESS: not relevant
      TELEX: 14-8367
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 5; Conservative
                                                                                                               LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 8 amino acids
                                                                                                                                                                                                         MOLECULE TYPE: peptide HYPOTHETICAL: NO
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MOLECULE TYPE: peptide
US-09-455-061-56
                                                                                                                                           amino acid
                                                                                                                                                                                 linear
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ZIP: 10020
COUNTRY: United States of America
ZIP: 10020
COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/376,372
FILING DATE:
CLASSIFICATION: 424
ATTONEY/AGENT INFORMATION:
NAME: Haley Jr. James F
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 21,794
REGISTRATION NUMBER: 21,794
REGISTRATION NUMBER: 21,794
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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; Sequence 1, Application US/08376372
; Patent No. 6306840
; GENERAL INFORMATION:
APPLICANT: Adams, Steven P
APPLICANT: Lin, Ko-Chung
APPLICANT: Lie, Wen-Cherng
APPLICANT: Castro, Alfredo C
APPLICANT: Zimmerman, Craig N
APPLICANT: Zimmerman, Craig N
APPLICANT: Hammond, Charles E
TITLE OF INVENTION: CELL ADHESION INHIBITORS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/498,237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                  APPLICATION:
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B190
TELECOMMUNICATION INFORMATION:
TELEPRONE: (212) 596-9000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TYPE: amino acids
TYPE: amino acids
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Best Local Similarity 100.
Matches 5, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION ATHEMA NEUROSCIENCES, INC.
TITLE OF INVENTION: INHIBITORS OF LEUKOCYTE ADHESION
NUMBER OF SEQUENCES: 157
CORRESPONDENCE ADDRESS:
ADDRESSEE: ATHEMA NEUROSCIENCES, INC.
STREET: 800 Gateway Blvd.
CITY: South San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08516
FILING DATE: 10-JUL-1995
CLASSIFICATION:
PRICE APPLICATION NUMBER: US 08/273,055
FILING DATE: 11-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: MOOI, LESLIE A.
REFERENCE/DOCKET NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 002010-008
TELECOMMULICATION:
TELECOMMULICATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
                                                                                                                                                                                                                  OTHER INFORMATION: Synthetically generated peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 23; DB 5; I ilarity 100.0%; Pred. No. 1.9e+05; Conservative 0; Mismatches 0;
PRIOR APPLICATION NUMBER: US 08/376, 372
PRIOR FILING DATE: 1995-01-23
NUMBER OF SEQ ID NOS: 5
SEQ ID NO 1
LENGTHARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application PC/TUS9508516 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (415) 877-3620 INFORMATION FOR SEQ ID NO: 3 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 5; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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USA
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US-08-271-830-101
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Ralease #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/039,780A

FILING DATE: 16-Mar-1998

CLASSIFICATION: <UNKNOWN>

ATTORNEY/AGENT INFORMATION:

NAME: SULLIVAN, SALLY A.

RESISTRATION NUMBER: 32,064

REFERENCE/DOCKET NUMBER: 32.95C

TELECOMMINICATION: INFORMATION:
                                         GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
HAWLEY-NELSON, PAMELA
APPLICANT: HAWLEY-NELSON, PAMELA
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL OF INA
TITLE OF INVENTION PEPTIDE-ENHANCED TRANSFECTIONS
NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS
HADDRESSER GREENLEE, WINNER & SULLIVAN
STREET: 5370 MANHATTAN CIRCLE, SUITE 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 23; DB 4; Length 8; 100.0%; Pred. No. 1.9e+05; rive 0; Mismatches 0; Indels
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APPLICANT: Zimmerman, Craig N.
APPLICANT: Hammond, Charles E.
APPLICANT: Hammond, Charles E.
APPLICANT: Cuervo, Julio Hernan
APPLICANT: Singh, Juswinder
ITILE OF INVENTION: CELL ADHESION INHIBITORS
FILE REFERENCE: 10274-023002
CURRENT APPLICATION NUMBER: US/08/875,321
CURRENT FILING DATE: 1997-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-09-039-780A-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (303)499-8080
TELEFAX: (303)499-8089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08875321
Patent No. 6376538
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Adams, Steven P. APPLICANT: Lin, Ko-Chung APPLICANT: Lee, Wen-Cherng APPLICANT: Castro, Alfredo C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100...
S; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ropology: linear
                                                                                                                                                                                                                                                                                                                                                                             CITY: BOULDER
    RESULT 32
US-09-039-780A-48
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FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/814,873
FILING DATE: December 24, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/402,389
FILING DATE: September 1, 1989
ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: peptide US-08-435-286-3
COMPUTER READABLE FORM:
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US-08-338-282-6
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                      GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kogan, Timothy P.
APPLICANT: Ren, Kaijun
APPLICANT: Vanderslice, Peter
APPLICANT: Vanderslice, Peter
APPLICANT: Vanderslice, Peter
TITLE OF INVENTION: INTEGRIN '4 1 TO VCAM OR FIBRONECTIN AND
TITLE OF INVENTION: LINBAR PEPTIDES THEREFOR
MUMBER OF SEQUENCES: ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Shore & Milnamow, Ltd.
STREET: 180 No. 5510332th Stetson, Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ## Sequence 3, Application US/08435286

## Sequence 3, Application US/08435286

## Patent No. 5688913

## APPLICANT: Arrhenius, Thomas S.

## APPLICANT: Arrhenius, Thomas S.

## APPLICANT: Gaeta, Federico C.A.

## TITLE OF INVENTION: CS-1 PEPTIDOMIMETICS, COMPOSITIONS AND TITLE OF INVENTION: METHODS OF USING THE SAME

## NUMBER OF SEQUENCES 15

## CORRESPED Dresseler, Goldsmith, Shore & Milnamow, Ltd.

## CITY: Chicago

## CITY: Chicago

## CITY: Chicago

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## CITY: Chicago

## CITY: Chicago

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/271,830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Modified-site
LOCATION: 10
OUTER INFORMATION: /label= Xaa
OTHER INFORMATION: /note= "Xaa=Thr-NH2."
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TELING DATE:
CLASSIPICATION: 435
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5510332thrup, Thomas E.
REGISTRATION NUMBER: 33,268
TELEPHONE: (312)616-5400
; TELEPHONE: (312)616-5400
; INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTER.STICS:
LENGTH: 10 amino acids
; TYPE: amino acids
; TYPE: amino acid
; TOPOLOGY: linear
TOPOLOGY: linear
Sequence 101, Application US/08271830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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STATE: II
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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Sequence 6, Application US/08338282
Patent No. 2730978
GENERAL INFORMATION:
APPLICANT: WAYNEY, B.A.
TITLE OF INVENTION: INHIBITION OF LYMPHOCYTE ADHERENCE TO VASCULAR ENDOTHELIUM
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Christensen, O'Connor, Johnson and Kindness STREET: 2800 Pacific First Center, 1420 Fifth Avenue CITY: Seatle STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: SUNGEMO, JOHN, S.
REGISTRATION NUMBER: 34,446
REFERENCE/DOCKET NUMBER: CYTE-1-6162
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-206-682-8100; 1-206-224-0727 (direct)
TELEPRAX: 1-206-224-0779
TELERX: 4938023
COMPUTER: REALABLE FORM:

MEDIUM TYPE: FIDEDPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,286
FILING DATE:
APPLICATION NUMBER: US/08/164,101
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
TELEPHONE: (312)616-5400
ITELEPHONE: (312)616-5400
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LEMTH: 10 amino acids
MARCHARACTERISTICS:
LEMTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage
COMPUTER: IBM PC/386 Compatible
OPERATING SYSTEM: MS-DOS 4.01
SOFTWARE: Word for Windows-t
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338,282
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MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-923-026-3
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Patent No. 581391

GENERAL INFORMATION:

APPLICANT: Arthenius, Thomas S.

APPLICANT: Elices, Mariano J.

APPLICANT: Elices, Mariano J.

APPLICANT: Cango List

ITILE OF INVENTION: Compositions and Methods of Using Same NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores Lip

STREET: ADDRESSEE: Campbell & Flores Lip

STREET: San Diego

CITY: San Diego

STREET: California

COUNTRY: United States

ZIP: 22122
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                                                                                                                                                                         100.0%; Score 23; DB 1; Length 10; 100.0%; Pred. No. 9.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indela
                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: CAFOTION DATA:
APPLICATION NUMBER: US/08/483,077C
FILING DATE: O7-JUN-1995
CLASSIFICATION NUMBER: 31,815
RECASSIFICATION NUMBER: 31,815
RECASTRATION NUMBER: 31,815
RECERENCE/DOCKET NUMBER: 31,815
RECASTRATION INFORMATION:
TELEPHONE: (619) 535-8949
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
LENGTH: 10 amino acids
                                                                                                                                                                                                              0; Mismatches
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                                                                                         MOLECULE TYPE: peptide
DESCRIPTION: GPEIL DVPST
US-08-338-282-6
                                       10 amino acida
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Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
HOLECULE TYPE: peptide
US-08-483-077C-6
                                                         amino acid
                                                                               linear
                                                                                                                                                                                                                                                  1 EILDV 5
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US-08-519-109B-6
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                                   LENGTH:
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Patent No. 6103870
GENERAL INFORMATION:
APPLICANT: Blices, Mariano J.
APPLICANT: Elices, Mariano J.
TITLE OF INVENTION: CS-1 PEPTIDOMIMETICS, COMPOSITIONS AND TITLE OF INVENTION: METHODS OF USING THE SAME COMMESSEE: Dressler, Goldsmith, Shore & Milnamow, Ltd. STREET: 180 No. 6103870th Stetson, Suite 4700
STATE: IL.
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                                              APPLICANT: Elices, Mariano J.
APPLICANT: Elices, Mariano J.
APPLICANT: Zheng, Zhong-Li
TITLE OF INVENTION: CYCLIc CS-1 Peptidomimetics,
TITLE OF INVENTION: Cyclic CS-1 Peptidomimetics,
TITLE OF INVENTION: Compositions and Methods of Using Same
NUMBER OF SEQUENCES: 33
CORRESPED CAMPBENES:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STREET: California
COUNTRY: United States
ZIP: 92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 23; DB 2; Length 10; 100.0%; Pred. No. 9.7;
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APPLICATION NUMBER: US/08/519,109B
FILING DATE: 25-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-CY 1795
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Arrhenius, Thomas S.
Tempczyk, Anna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (619) 535-9001
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
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Best Local Similarity 100.
Matches 5; Conservative
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Sequence 3. Application PC/TUS9510811
Sequence 3. Application PC/TUS9510811
GENERAL INFORMATION:
APPLICANT: Cytel Corporation
TITLE OF INVENTION: Cyclic CS-1 Peptidomimetics,
TITLE OF INVENTION: Compositions and Methods For Using The Same
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CS-1 PEPTIDOMIMETICS, COMPOSITIONS AND METHODS OF USING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 23; DB 5; Length 10; Best Local Similarity 100.0%; Pred. No. 9.7; Matches 5; Conservative 0; Mismatches 0; Indels
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STATE: CALLICOTHIA
ZIP: 92122
COMPUTER READABLE FORM:
MEDTIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENT IN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10811
FILING DATE: 25-AUG-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: HOOK, Gregory R.
REGISTRATION NUMBER: 38.701
REFERENCE/DOCKET NUMBER: PP-CY 1778
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 3:
SEQUENCE CHRARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                   Sequence 3, Application PC/TUS9413943

GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: CS-1 PEPTIDOMIMETICS, COMPOSITIC
TITLE OF INVENTION: METHODS OF USING THE SAME
NUMBER OF SEQUENCES: 15
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/13943
FILING DATE: 5-DEC-1994
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTER.ESTICS:
TENDOR OF TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TENDOR TEND
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STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
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STATE: California
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                                              EILDV 5
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| Patent No. 6117840
| GENERAL INFORMATION:
| APPLICANT: Arrhenius, Thomas S.
| APPLICANT: Biles, Mariano J.
| APPLICANT: Gaeta, Federico C.A.
| TITLE OF INVENTION: CS-1 PEPTIDOMIMETICS, COMPOSITIONS
| TITLE OF INVENTION: AND METHODS OF USING THE SAME
| NUMBER OF SEQUENCES: 15
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Walsh & Katz, Ltd.
| STREET: 135 South La Salle Street, Suite 1625
| CTTY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 23; DB 3; Length 10; 100.0%; Pred. No. 9.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE:
CLASSIPICATION DATA:
FILING DATE:
CLASSIPICATION:
NAME: GAMBON:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPACH:
SEQUENCE (312) 781-9548
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-837-154-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/164,101
APPLICATION NUMBER: US/08/923,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                            ALICANAL FORMAT IN CONTROLL OF THE REGISTRATION NUMBER: 29,381
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)616-5400
TELEPHONE: (312)616-5400
TELEPAX: (312)616-5400
TELEPAX: (312)616-5400
TELEPAX: (312)616-5400
TELEPAX: (312)616-5400
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TELEPAX: (312)616-5400
TELEPAX: (312)616-5400
TELEPAX: (312)61
                                                                                                                                                                                                                      FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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STATE: IL
COUNTRY: UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EILDV 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-837-154-3
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us-09-251-073a-16.open.rai

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TELECOMMUNICATION INFORMATION:
TELEPAC. (216) 861-5582
TELEFAX: (216) 241-1666
TELEX: (216) 980162
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
 10-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: Amino Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: Peptide US-08-190-130-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Cleveland
STATE: Ohio
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 BILDV 5
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US-08-190-130-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: Peptide OTHER INFORMATION: derived from fibronectin'
                                                                                         100.0%; Score 23; DB 5; Length 10; 100.0%; Pred. No. 9.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 23; DB 3; Length 11; 100.0%; Pred. No. 11;
                                                                                                                               0; Indels
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                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08467580B
Patent No. 6001809
GENERAL INFORMATION:
APPLICANT: Thorsett. Eugene D
APPLICANT: Pleiss, Michael A
TILLE OF INVENTION: Inhibitors of Leukocyte Adhesion
FILE REFERENCE: 123-US-CIP1
CURRENT APPLICATION UNMBER: US/08/467,580B
CURRENT FILING DATE: 1995-06-06
EARLIER APPLICATION NUMBER: 08/273,055
EARLIER FILING DATE: 1994-07-11
NUMBER OF SEQ ID NOS: 163
SOFTWARE: PatentIn Ver. 2.0
IENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application PC/TUS9508516
GENERAL INFORMATION:
APPLICANT: ATHENA NEUROSCIENCES, INC.
TITLE OF INVENTION: INHIBITORS OF LEUKOCYTE ADHESION
NUMBER OF SEQUENCES: 157
CORRESPONDENCE ADDRESS:
ADDRESSEE: ATHENA NEUROSCIENCES, INC.
STREET: 800 Gateway Blvd.
CIT: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US95/08516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-08-467-580-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                             5; Conservative
             TOPOLOGY: linear
MOLECULE TYPE: peptide
amino acid
                                                                                                      Best Local Similarity
Matches 5; Conserva
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LOCATION: (1)
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4 EILDV 8
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PCT-US95-08516-2
                                                      PCT-US95-10811-3
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                                                                                         Query Match
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Patent No. 5628979

GENERAL INFORMATION: Alan William John

TITLE OF INVENTION: No. 5628979el Reagent For Tumour

TITLE OF INVENTION: Inaging and Therapy

NUMBER OF SEQUENCES:

ADDRESSEE: Fay, Sharpe, Beall, Fagan,

ADDRESSEE: Minnich & McKee

STREET: Suite 700

STREET: Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/273,055
FILING DATE: 11-JUL-1994
ATTORNEY/ACENT INFORMATION:
NAME: MOCI, LESLIE A.
REGISTRATION NUMBER: 002010-008
FELECOMMUNICATION INFORMATION:
FELECOMMUNICATION INFORMATION:
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ZIP: 44114-2518
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
MEDIUM TYPE: 720 KD storable
COMPUTER: 120 KD storable
COMPUTER: 120 KD storable
COMPUTER: 120 KD storable
COMPUTER: 120 KD storable
COMPUTER: 120 KD storable
COMPATION NUMBER: 13 1994
CLASSIFICATION NUMBER: US/08/190,130
FILING DATE: June 13, 1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Minnich, Richard J.
RESISTRATION NUMBER: 24,175
RESISTRATION NUMBER: 24,175
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Sequence 9, Application US/08483077C
| Patent No. 5811391
| GENERAL INFORMATION:
| APPLICANT: Arrhenius, Thomas S. APPLICANT: Tempczyk, Anna
| APPLICANT: Tempczyk, Anna
| APPLICANT: Tempczyk, Anna
| APPLICANT: Elices, Mariano J. APPLICANT: Elices, Mariano J. APPLICANT: Cyclic Cs-I Peptidomimetics,
| TITLE OF INVENTION: Cyclic Cs-I Peptidomimetics,
| TITLE OF INVENTION: Compositions and Methods of Using Same
| TITLE OF INVENTION: Compositions and Methods of Using Same
| TITLE OF INVENTION: Compositions and Methods of Using Same
| TITLE OF INVENTION: Compositions and Methods of Using Same
| TITLE OF INVENTION: Compositions and Methods of Using Same
| TITLE OF INVENTION: Compositions and Methods of Using Same
| TITLE OF INVENTION: Campbell & Flores LLP
| STREEF: Campbell & Flores LLP
| STREEF: Callifornia
| STREEF: Callifornia
| STREEF: Callifornia
| STREEF: Callifornia
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2800 Pacific First Center, 1420 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Sundamo, John, S.
REGISTRATION NUMBER: 34,446
REFERENCE/DOCKET NUMBER: CTTE-1-6162
REPERENCE/COCKET NUMBER: CTTE-1-6162
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-206-682-8100; 1-206-224-0727 (direct)
TELEFAX: 1-206-224-0779
                                                                                 COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage
COMPUTER: IBM PC/386 Compatible
OPERATING SYSTEM: MS-DOS 4.01
SOPTWARE: Word for Windows-t
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338,282
FILING DATE:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,077C
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
DESCRIPTION: 812; Fig. 9B;LHGPE ILDVP ST
                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/814,873
FILING DATE: December 24, 1991
PRIOR APPLICATION NUMBER: 07/402,389
FILING DATE: September 1, 1989
ATTORNEY/AGENT INFORMATION:
NAME: Sundsmo, John, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 92122
COMPUTER READABLE FORM:
CMBUUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
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INFORMATION FOR SEQ ID NO:
                                               Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                     COUNTRY:
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GENERAL INFORMATION:
APPLICANT: Wayner, E.A.
TITLE OF INVENTION: INHIBITION OF LYMPHOCYTE ADHERENCE TO VASCULAR ENDOTHELIUM
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
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                                                                     Gaps
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                   ; DB 1; Length 12;
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                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Dressler, Goldsmith, Shore & Milnamow, Ltd. 180 No. 5688913th Stetson, Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER PRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,286
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/164,101
APPLICATION NUMBER: US/08/164,101
                                                                                                                                                                                                                                                                             Sequence 2, Application US/08435286

Patent No. 568913

GENERAL INFORMATION:
APPLICANT: Arrhenius, Thomas S.
APPLICANT: Blices, Mariano J.
TITLE OF INVENTION: Geter. Federico C.A.
TITLE OF INVENTION: METHODS OF USING THE SAME
NUMBER OF SEQUENCES:
CORRESONDENCES:
ADDRESSEE: Dressler, Goldsmith, Shore & Milname
                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                   100.0%; Score 23; 100.0%; Pred. No. :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Gameon, Edward P.
REGISTRATION UNUBER: 29,381
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)616-5460
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 48
US-08-338-282-5
Sequence 5, Application US/08338282
; Patent No. 5730978
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ATTORNEY/AGENT INFORMATION:
                                          Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: peptide US-08-435-286-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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CITY: Chicago
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US-08-435-286-2
                      Query Match
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Sequence 2, Application US/08923026
Patent No. 6103870
GENERAL INFORMATION:
APPLICANT: Arrhenius, Thomas S.
APPLICANT: Blices, Mariano J.
APPLICANT: Gaeta, Federico C.A.
TITLE OF INVENTION: CS-1 PEPTIDOMIMETICS, COMPOSITIONS AND TITLE OF INVENTION: METHODS OF USING THE SAME NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Dressler, Goldsmith, Shore & Milnamow, STREET: 180 No. 6103870th Stetson, Suite 4700 CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/164,101
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Gameon, Edward P.
REGISTRATION NUMBER: 29, 381
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (312)616-5400
TELEPRA: (312)616-5460
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
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3Y: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60601
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US-08-837-154-2
                                                                                                        RESULT 51
US-08-923-026-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Arrhenius, Thomas S.
APPLICANT: Tempczyk, Anna J.
APPLICANT: Tempczyk, Anna J.
APPLICANT: Blices, Mariano J.
APPLICANT: Blices, Mariano J.
APPLICANT: Blices, Mariano J.
TITLE OF INVENTION: Cyclic Cs-1 Peptidomimetics,
TITLE OF INVENTION: Compositions and Methods of Using Same
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
GITY: San Diego
STATE: California
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 23; DB 2; Length 12; 100.0%; Pred, No. 12;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/519,109B
FILING DATE: 25-AUG-1995
CLASSIPICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUWBER: 31, 315
REFERENCE/DOCKET NUMBER: P-CY 1647
TELECOWMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-9001
TELEPAX: (619) 535-9001
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
NOLECTLE TYPE: peptide
US-08-483-077C-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-CY 1795
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
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100.0%; Score 23; DB 3; Length 12; 100.0%; Pred. No. 12;
                                           0; Indels
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Patent No. 6117840
GENERAL INFORMATION:
APPLICANT: Arrhenius, Thomas S.
APPLICANT: Elices Mariano J.
APPLICANT: Gaeta, Pederico C.A.
TITLE OF INVENTION:
TITLE OF INVENTION: AND METHODS OF USING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Katz, Ltd.
STREET: 135 South La Salle Street, Suite 1625
                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Chicago
STATE: IL
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APPLICANT: Cytel Corporation
TITLE OF INVENTION: Cyclic CS-1 Peptidomimetics,
TITLE OF INVENTION: Compositions and Methods For Using The Same
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                           CS-1 PEPTIDOMIMETICS, COMPOSITIONS AND METHODS OF USING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 23; DB 5; Length 12;
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 4370 La voll.
STREET: 4370 La voll.
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 91.22
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10811
TITING DATE: 25-AUG-1995
                                                                                                 TITLE OF INVENTION: CS-1 PEPTIDOMIMETICS, COMPOSITIC TITLE OF INVENTION: METHODS OF USING THE SAME NUMBER OF SEQUENCES: 15
COMPUTER TEADABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OFFRAING SYSTEM: PC-DOS/MS-DOS SOFFWARE: PATENTIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US94/13943 FILING DATE: 5-DCC-1994
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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NAME: HOOK, Gregory R.
REGISTATION NUMBER: 38,701
REPERBUEL/DOCKET NUMBER: FP-CY 1778
TELECOMMUNICATION INFORMATION:
Sequence 2, Application PC/TUS9413943
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application PC/TUS9510811
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%;
Matches 5; Conservative 0;
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TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 12 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 amino acids
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LENGTH: 12 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US94-13943-2
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TOPOLOGY: linear
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MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible OPERALING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO) CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/424,656
FILING DATE: PRING PATA:

PRILING DATE: 29-MAY-1997
INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 12 amino acids

TYPE: amino acid

TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels
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                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/837,154
                                                                                                                                                                                                                                     APPLICAL.
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INPORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
TELECOMMUNICATION INPORMATION:
TELEFAX: (312)781-9470
TELEFAX: (312)781-9548
JINFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHRACATERISTICS:
LENGTH: 12 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
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Patent No. 6458026
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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Length 12;

Score 23; DB 5; Pred. No. 12;

100.0%;

Query Match Best Local Similarity

RESULT 54

Gaps

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US-08-701-124-59
is Sequence 59, Application US/08701124
is Patent No. 5846782
is GENERAL INFORMATION:
APPLICANT: Wickham, Thomas J.
APPLICANT: Roelvink, Petrus W.
TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF TITLE OF INVENTION: CONSTRAINED PEPTIDE MOTIPS
invines OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza - 49th Ploor CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 23; DB 2; Length 21; constructive 100.0%; Pred. No. 21; Conservative 0; Mismarcher
                                                         Query Match 100.0%; Score 23; DB 2; Length 21; Best Local Similarity 100.0%; Pred. No. 21; Matches 5; Conservative 0; Mismatches 0; Indels
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Patent No. 6057155

GENERAL INFORMATION:
APPLICANT: Wickham, Thomas J.
APPLICANT: Woesdi, Imre
TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
TITLE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza - 49th Floor
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/701,124 FILING DATE: 21-AUG-1996 INFORMATION FOR SEQ ID NO: 59:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 21 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acida
, MOLECULE TYPE: peptide US-08-701-124-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide US-08-701-124-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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Best Local Similarity
Matches 5; Conserv
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, OTHER INFORMATION: Description of Artificial Sequence: Linker
US-09-367-953B-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 23; DB 4; Length 18; 100.0%; Pred. No. 18; tive 0; Mismatches 0; Indels
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Patent No. 5846782

GENERAL INFORMATION:
APPLICANT: Wickham, Thomas J.
APPLICANT: Roelvink, Petrus W.
APPLICANT: Roelvink, Petrus W.
APPLICANT: Roelvink, Petrus W.
APPLICANT: Roelvink, Petrus W.
APPLICANT: Roelvink, Petrus W.
APPLICANT: Roelvink, Petrus W.
APPLICANT: Roelvink, Petrus W.
APPLICANT: Roelvink, Petrus W.
APPLICANT: ROELVINK:
APPLICANT: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza - 49th Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
  0; Indels
                                                                                                                                                                     Sequence 25, Application US/09367953B
; Sequence 25, Application US/09367953B
; Patent No. 629752
; GENERAL INFORMATION:
; APPLICANT: Kingsman, Alan J
; APPLICANT: Kingsman, Susan M
; TITLE OF INVENTION: Anti-HIV peptides and proteins
; FILE REFERENCE: 550-154
; CURRENT APPLICATION NUMBER: US/09/367,953B
; CURRENT FILING DATE: 1999-08-24
; PRIOR FILING DATE: 1999-02-23
; PRIOR FILING DATE: 1999-02-24
; RINGR APPLICATION NUMBER: GB 9703802.0
; PRIOR FILING DATE: 1997-02-24
; NUMBER: OF SEQ ID NOS: 131
; SEQ ID NO 25
; LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/701,124
FILING DATE: 21-AUG-1996
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERIFICS:
LENGTH: 21 amino acida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
5; Conservative
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STRANDEDNESS: sir
                                                                                                                                            RESULT 56
US-09-367-953B-25
                                         1 EILDV 5
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US-08-701-124-57
Matches
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USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 59, Application US/09130225
; Betent No. 6057155
; Patent No. 6057155
; GENERAL INFORMATION:
   APPLICANT: Wickham, Thomas J.
   APPLICANT: Kovedi, Imre
   TILE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
   TILE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS
; NUMBER OF SEQUENCES: 80
   CORRESPONDENCE ADDRESS:
   ADDRESSEE: Leydig, Voit & Mayer, Ltd.
   STREET: Two Prudential Plaza - 49th Floor
   CITY: Chicago
   STATE: Illinois
   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/130,225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 60601

ZIP: 60601

MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATR:
APPLICATION NUMBER: US/09/130,225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                               FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 8-701124
FILING DATE: 21-846-1996
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 8-701124
FILING DATE: 21-AUG-1996
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear;
; MOLECULE TYPE: peptide
US-09-130-225-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
GY: linear
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Matches 5; Conserve
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US-09-130-225-59
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US-09-455-061-59
is Sequence 59, Application US/09455061
j Patent No. 6329190
j GENERAL INFORMATION:
j APPLICANT: Wickham, Thomas J.
APPLICANT: Roelvink, Petrus W.
APPLICANT: Kovesdi, Imre
j TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF TITLE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS
CORRESPONDENCE ADDRESSE: Levydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza - 49+h ---
CITY: Chicago
STATE: Illinoi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 23; DB 4; Length 21;
Pred. No. 21;
                                                                     APPLICANT: Wickham, Thomas J.
APPLICANT: Roelvink, Petrus W.
APPLICANT: Roelvink, Petrus W.
APPLICANT: Roelvink, Petrus W.
APPLICANT: Roelvink, Petrus W.
APPLICANT: Roelvink, Petrus W.
TITLE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS
TUTLE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS
TUTLE OF INVENTION: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza - 49th Floor
CITY: Chicago.
STATE: Illinois
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CURRENT APPLICATION DATA:

APPLICATION NUMBER:
FILING DATE: 06-DEC-1999
PRIOR APPLICATION NUMBER: US 9-130225
FILING DATE: 06-AUG-1999
PRIOR APPLICATION NUMBER: US 9-130225
FILING DATE: 06-AUG-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 8-701124
FILING DATE: 21-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hefner, M. Daniel
REGISTRATION NUMBER: 41,826
REFERENCE/DOCKET NUMBER: 203128
INFORMATION FOR SEQ ID NO: 57:
SEQUINCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
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                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 57, Application US/09455061
Patent No. 6329190
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%;
Matches 5; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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100.0%; Score 23; DB 1; Length 24; 100.0%; Pred. No. 24;
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Best Local Similarity 100.0%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/08291349A
Patent No. 5545620
GENERAL INFORMATION:
APPLICANT: Wall, Sharon M.
APPLICANT: MCCarthy, James B.
APPLICANT: Furcht, Leo T.
TITLE OF INVENTION: Inhibitors of Retroviral Infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
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COMPUTER: Floppy disk
COMPUTER: Floppy disk
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/006,121
FILING DATE: 19 JAN 1993
CLASSIFICATION NUMBER: 08/006,121
FILING DATE: 19 JAN 1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John J.
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,673-B
TELEFOOMMULICATION INFORMATION:
TELEFOOMMULICATION: 1312-715-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Peptide
LOCATION: 1..25
OTHER INFORMATION: /note= "FN6 (1961-1985)
OTHER INFORMATION: fibronectin fragment : CS-1"
                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS: ADDRESSEE: Allegretti & Witcoff STREET: 10 S. Wacker Drive CITY: Chicago STATE: 111inois
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-453-378-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO.
SEQUENCE CHARACTERRISTICS:
LENGTH: 25 amino acids
                                                                                                                                                                              Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                     17 EILDV 21
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                                                                                                                                                      Query Match
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Sequence 2, Application US/08453378

Patent No. 561646

GENERAL INFORMATION:

APPLICANT: Salmi, Marko

APPLICANT: Salmi, Marko

APPLICANT: Salmi, Marko

APPLICANT: Jalkanen, Sirpa

TITLE OF INVENTION: Compositions And Diagnostic Methods

TITLE OF INVENTION: Using Monoclonal Antibodies Against CD44v6

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSES: Sterne, Kessler, Goldstein & Fox

STRET: 1100 New York Avenue Suite 600

CITY: Washington

STRET: 1100 New York Avenue Suite 600

CITY: Washington

STRET: 1100 New York Avenue Suite 600

COUNTRY: U.S.A.

ZIP: Z0005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATION SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/453,378

FILING DATE:

CLASSIFICATION NUMBER: US/08/453,378

FILING DATE:

FILING DATE:

REFERENCE/OMMUTICATION HUMBER: 1102.0070000

TELECOMMUTICATION HUMBER: 1102.0070000

TELECOMMUTICATION HUMBER: 1102.0070000
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                                                                                                            CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/455,061
FILING DATE: 06-DEC-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 9-130225
FILING DATE: 06-AUG-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 8-701124
FILING DATE: 10-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hefner, M. Daniel
REGISTRATION NUMBER: 203128
INFORMATION FOR EN 10 NO: 59:
CENGRATION NUMBER: 203128
INFORMATION FOR EN IN NO: 59:
CENGRATION CATA
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-455-061-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 5; Conservative
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TITLE OF INVENTION: Imaging and Therapy
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STRANDEDNESS: Siz
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 EILDV 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
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                                                                                                                                                                    APPLICANT: Allen Janice B.
APPLICANT: Allen Janice B.
APPLICANT: Allen Janice B.
APPLICANT: Allen Janice B.
APPLICANT: Wall, Sharon M.
APPLICANT: Wall, Sharon M.
TITLE OF INVENTION: Method for Treating Acute and
TITLE OF INVENTION: With Fibronectin Activity
NUMBER OF SEQUENCES: 6
CORRESPONDENCES: 6
CORRESPONDENCES: 8
ADDRESSEE: Merchant & Gould
STREET: 3100 No. 5591719west Center
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gapa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 23; DB 1; Length 25, 100.0%; Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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No. 5628979el Reagent For Tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/990,296
FILING DATE: 19921210
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kowalchyk, Alan W.
REGISTRATION NUMBER: 31,535
REFERENCE/DOCKET NUMBER: 600.252-US-01
TELEPHONE: 612-332-9081
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acid residues
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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FRAGMENT TYPE: Internal Fragment
ORIGINAL SOURCE: Synthetically Derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 55402
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 66
US-08-190-130-1
; Sequence 1, Application US/08190130
; Patent No. 5628979
; GENERAL INFORMATION:
APPLICANT STUTTLE, Alan Willian
; TITLE OF INVENTION: No. 56289796
                                                                                                                   Sequence 4, Application US/07990296
Patent No. 5591719
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 5; Conservative
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                  18 EILDV 22
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COCATION:
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COCATION:
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NAME/KEY:
NAME/KEY:
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                                                                                              US-07-990-296-4
                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
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Gaps
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Best Local Similarity 100.0%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches no Train
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHER OF SEQUENCES: GORRESPONDENCE ADDRESS:
ADDRESSEE: Fay, Sharpe, Beall, Fagan, ADDRESSEE: Minnich & McKee
STREET: 1100 Superior Avenue
STREET: 1100 Superior Avenue
STREET: 0010
CITY: Cleveland
COWTRY: U.S.A.
ZIP: 44114-2518
COMPUTER READABLE FORM:
MEDLING TYPE: Diskette, 3.50 inch, MEDLING TYPE: Diskette, 3.50 inch, MEDLING TYPE: Diskette, 3.50 inch, MEDLING TYPE: Diskette, 3.50 inch, MEDLING TYPE: Diskette, 3.50 inch, MEDLING SYSTEM: DOS 5.0
SOFTWARE: Nord Perfect 5.1
CURRENT APPLICATION DATA: DAFA: ATTORNEY/AGENT INFORMATION: 02/04/175
REGISTRATION NUMBER: 24,175
REGISTRATION NUMBER: 24,175
REGISTRATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORM: (216) 861-5582
TELEFORM: (216) 861-5582
                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: (216) 980162
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: Peptide
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Patent No. 5736978
GENERAL INFORMATION:
APPLICANT: Wayner, B.A.
TITLE OF INVENTION: INHIBITION OF LYMPHOCYTE ADHERENCE TO VASCULAR ENDOTHELIUM
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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CS-1 domain; Fig. 9A,DELPQ LVTLP HPNLH GPEIL DVPST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
STREET: 2800 Pacific First Center, 1420 Fifth Avenue
                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Sundsmo, John, S.
REGISTRATION NUMBER: 34,446
REFERNCE/DOCKET NUMBER: CYTE-1-6162
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-206-682-8100; 1-206-224-0727 (direct)
TELEPRAX: 1-206-224-0779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage
                              Pred. No. 26;
                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Word for Windows-t
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338,282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/814,873
FILING DATE: December 24, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/402,389
FILING DATE: September 1, 1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC/386 Compatible OPERATING SYSTEM: MS-DOS 4.01
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08338282
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INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
TOPOLOGY: linear
                       Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 5; Conserv
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DESCRIPTION:
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                                                                                                                  1 EILDV 5
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Sequence 1, Application US/08435286

Sequence 1, Application US/08435286

Patent No. 568933

PAPELICANT: Arrhenius, Thomas S.

APPLICANT: Blices, Mariano J.

APPLICANT: Gata, Federico C.A.

TITLE OF INVENTION: CS-1 PEPTIDOMIMETICS, COMPOSITIONS AND TITLE OF INVENTION: METHODS OF USING THE SAME

NUMBER OP SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSE: Dressler, Goldsmith, Shore & Milnamow, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 25; 26;
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STREET: 180 No. 5688913th Stetson, Suite 4700
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 23; Best Local Similarity 100.0%; Pred. No. 2 Matches 5; Conservative 0; Mismatche
             FILING DATE: June 13, 1994
CLASSIFICATION: 424
ATTORNEY, AGENT INPORMATION:
NAME: Minnich, Richard J.
REGISTRATION NUMBER: 24,175
REFERENCE/DOCKET NUMBER: 24,175
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 861-5582
TELEFAX: (216) 861-5582
TELEFAX: (216) 241-1666
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 25
LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: IL
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/164,101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)616-5400
TELEFAX: (312)616-5460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (312)616-5460
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
US-08-190-130-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: Amino Acid
STRANDEDNESS: Sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 EILDV 22
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Gaps
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Patent No. 5824547

GENERAL INFORMATION:
APPLICANT: HASHINO, Kimikazu
APPLICANT: MATGUSHITA, Hideyuki
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: METHOD OF PRODUCTION OF TRANSFECTED CELLS
NUMBER OF SEQUENCES:
ADDRESSED:
ADDRESSED:
Browdy and Neimark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 23; DB 2; Length 25; 100.0%; Pred. No. 26; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O'BERATING SYSTEM: FC-LUDS/MS-LUOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,854
FILING DATE:
FLING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/JD95/02425
FILING DATE: 29-NOV-1995
PRIOR APPLICATION NUMBER: 317721/1994
FILING DATE: 29-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAMME: BLOWDY, ROGET L.
REGISTRATION NUMBER: 45,618
REGISTRATION NUMBER: 25,618
REGISTRATION NUMBER: 25,618
REGISTRATION NUMBER: 25,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEPHONE: (202) 737-3528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                       APPLICATION NUMBER: US/08/483,077C
GLASSIFICATION NUMBER: US/08/483,077C
GLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REGISTRATION INFORMATION:
TELECHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20004
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 10v.v
Si Conservative
                                         CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 EILDV 22
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US-08-836-854-2
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Patent No. 5811391

GENERAL INFORMATION:
APPLICANT: Tempczyk, Anna
APPLICANT: Tempczyk, Anna
APPLICANT: Tempczyk, Anna
APPLICANT: Tempczyk, Anna
APPLICANT: Zheng, Zhong-Li
TITLE OF INVENTION: Cyclic CS-1 Peptidomimetics,
TITLE OF INVENTION: Cyclic CS-1 Peptidomimetics,
TITLE OF INVENTION: Compositions and Methods of Using Same
CORESPONDENCES: 33
CORESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LiP
STREET 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
CITY: San Diego
CUNTR: California
COUNTR: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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APPLICANT: Shifferli, Kevin P.
TITLE OF INVENTION: Peptide-Enhanced Cationic Lipid
TITLE OF INVENTION: Transfections
NUMBER OF SIQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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COMPUTER: Tabopy disk

COMPUTER: TBM PC compatible

COMPUTER: TBM PC compatible

COMPUTER: TBM PC compatible

COMPUTER: Datentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/658,130

FILING DATE: 04-JUN-1996

CLASSIFICATION DATA:

APPLICATION NUMBER: US 08/477,354

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INPORMATION:

NAME: CARLULARS, Jennie M.

REGISTRATION NUMBER: 34,464

REGISTRATION NUMBER: 34,464

REGISTRATION NUMBER: 34,464

REGISTRATION NUMBER: 34,964

RELEPAN: (303) 499-8089

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 amino acids

LENGTH: 25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SS: single
not relevant
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Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                        ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: sir
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Patent No. 5958874
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Clark, Richard A
APPLICANT: Grailing, Doris
APPLICANT: Gailit, James
TITLE OF INVENTION: EXCOMBINANT FIBRONECTIN-BASED
TITLE OF INVENTION: EXTRACELLULAR MATRIX FOR WOUND HEALING
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 23; DB 2; Length 25; 100.0%; Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSE: Jaeckle Fleischmann & Mugel, LLP
STREET: 39 State Street
CITY: Rochester
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (19) 535-8949
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: peptide US-08-519-109B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 14614-1310
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Furcht, Leo T.
APPLICANT: McCarthy, James B.
APPLICANT: Wahl, Sharon M.
APPLICANT: Wahl, Sharon M.
APPLICANT: Allen, Janice B.
APPLICANT: Billups, Kevin L.
APPLICANT: Brocett, Jeffrey E.
TITLE OF INVENTION: Method for Treating Inflammatory
TITLE OF INVENTION: Diseases Using Polypeptides with Fibronectin Activity
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Comits
STREET Merchant & Comits
STREET Merchant & Comits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                               Gaps
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STREET: 90 South 7th Street, 3100 No. 5840691west Center
CHTY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 23; DB 2; Length 25; 100.0%; Pred. No. 26; tive 0; Mismatches 0; Indels
                                                                                           Query Match 100.0%; Score 23; DB 2; Length 25; Best Local Similarity 100.0%; Pred. No. 26; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY.

ZIP: 55402

ZIP: 55402

COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATCHILIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/480,133A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 514

PRIOR APPLICATION NUMBER: US/08/139,903

FILING DATE: 21-OCT-1993

PRIOR APPLICATION NUMBER: US/08/139,903

FILING DATE: 21-OCT-1993

PRIOR APPLICATION NUMBER: US/09/0,296

FILING DATE: 10-DEC-1993

ATPLICATION NUMBER: US/09/0,296

FILING DATE: 10-DEC-1993

ATPLICATION NUMBER: US/07/990,296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           600-308US01
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08480133A Patent No. 5840691 GENERAL INFORMATION. APPLICANT: MCCarthy, James B. APPLICANT: MCCarthy, James B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 600
TELECOMMUNICATION
TELEPHONE: 612-332-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 5; Conservative
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MOLECULE TYPE: peptide

// MOLECULE TYPE: peptide
US-08-836-854-2
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STRANDEDNESS:
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18 EILDV 22
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Gaps

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0; Indels

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COPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/09/025,706
FILING DATE:
CLASSIFICATION:
APPLICATION NUMBER: 34,103
REGISTRATION NUMBER: 34,103
REGISTRATION NUMBER: 87653.97R263
FEBEROME - 716-262-3640
FILECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 4:
FEBEROME: 716-262-3640
FILENGTH: 25 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
FILENGTH: 25 amino acids
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FILENGTH: 25 amino acids
FILENGTH: 26 amino acids
FILENGTH: 2706-4
FILENGTH: 300.08; Force 23; DB 2; Length 25;
Best Local Similarity 100.08; Pred: No. 26;
Best Local Similarity 00.08; Pred: No. 26;
Best Local Similarity 00.08; Pred: No. 26;
Matches 5; Conservative 0; Mismatches 0; Indels 0;
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Search completed: February 8, 2003, 10:25:20 Job time : 16 secs

1 EILDV 5 ||||| 18 EILDV 22

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